

Fig. 1a

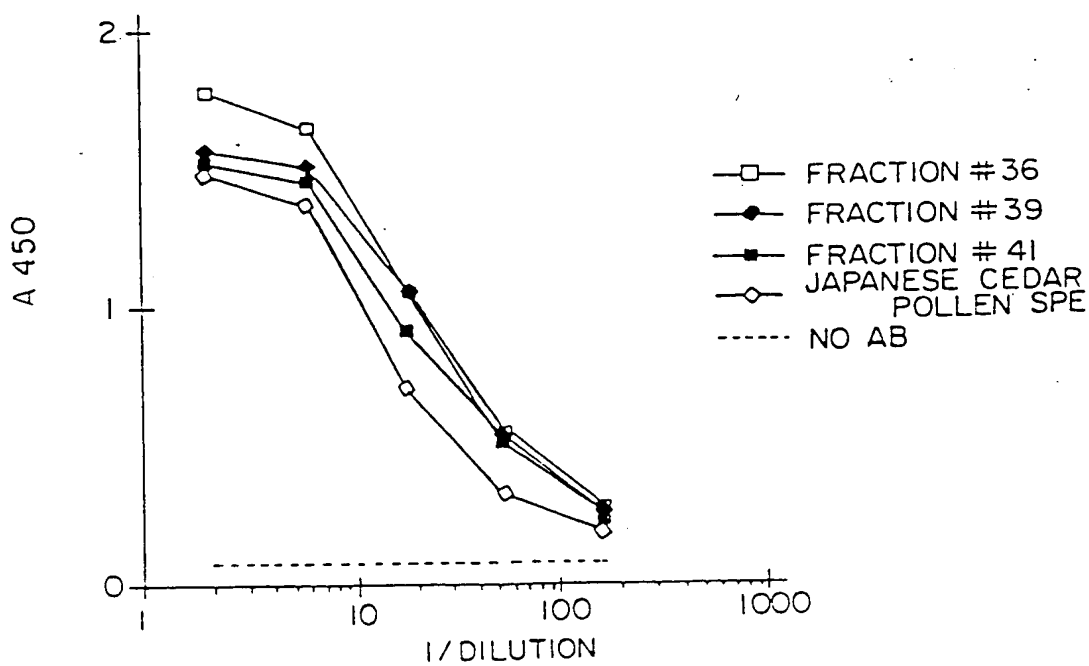


Fig. 3

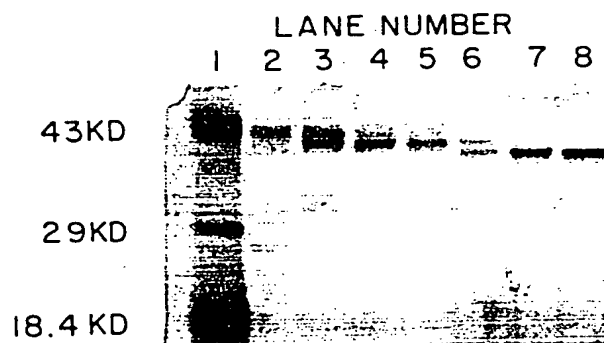


Fig. 1b

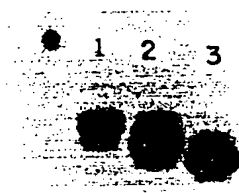


Fig. 2

5' -AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATCTACA CTCTGCTACC 60

AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT 107
Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
-21 -20 -15 -10

GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA 155
Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
-5 1 5

GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA 203
Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
10 15 20 25

GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GAT CTT TAT 251
Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
30 35 40

ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT 299
Thr Val Thr Asn Ser Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
45 50 55

CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT 347
Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
60 65 70

Fig. 4

395 GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGC TAT
 Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr
 75 80 85
 443 AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT
 Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly
 90 95 100 105
 491 CCC TGT GTG TTT ATC AAG AGA GGT AGC AAT GTT ATC ATA CAC GGT TTG
 Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu
 110 115 120
 539 TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC
 Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn
 125 130 135
 587 GAG AGT TTT GGG GTG GAG CCT GGT CAT CCT CAG GAT GGC GAT GCT CTT
 Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu
 140 145 150
 635 ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC
 Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser
 155 160 165

Fig. 4 cont.

AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT	683
Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val	185
170	180
ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA	731
Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu	200
190	195
GGG CAT GAT GAT GCA TAT AGT GAT GAT GAC AAA TCC ATG AAG GTG ACA GTG	779
Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val	215
205	210
GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA	827
Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala	230
220	225
CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT	875
Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr	245
235	240
ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG	923
Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly	265
250	255

Fig. 4 cont.

AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG AAG CAA GTA ACC ATA 971
 Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile 280
 270 275
 CGT ATT GGA TGC AAA ACA TCA TCT TGT TCA AAT TGG GTG TGG CAA 1019
 Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln 295
 285 290
 TCT ACA CAA GAT GTT TTT TAT AAT GGA GCT TAT TTT GTA TCA TCA GGG 1067
 Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly 310
 300 305
 AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT 1115
 Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val 315 320 325
 GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA 1163
 Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu 340 345
 330 335
 ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC 1217
 Thr Cys Ser Leu Ser Lys Arg Cys 350
 TATCTAAATT AACATCAACA AGAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA 1277
 AATAAAAATG TATCTTTTAC TATTAAAAA AAAAATGATC GATCGGACGG TACCTCTAGA-3' 1337

Fig. 4 cont.

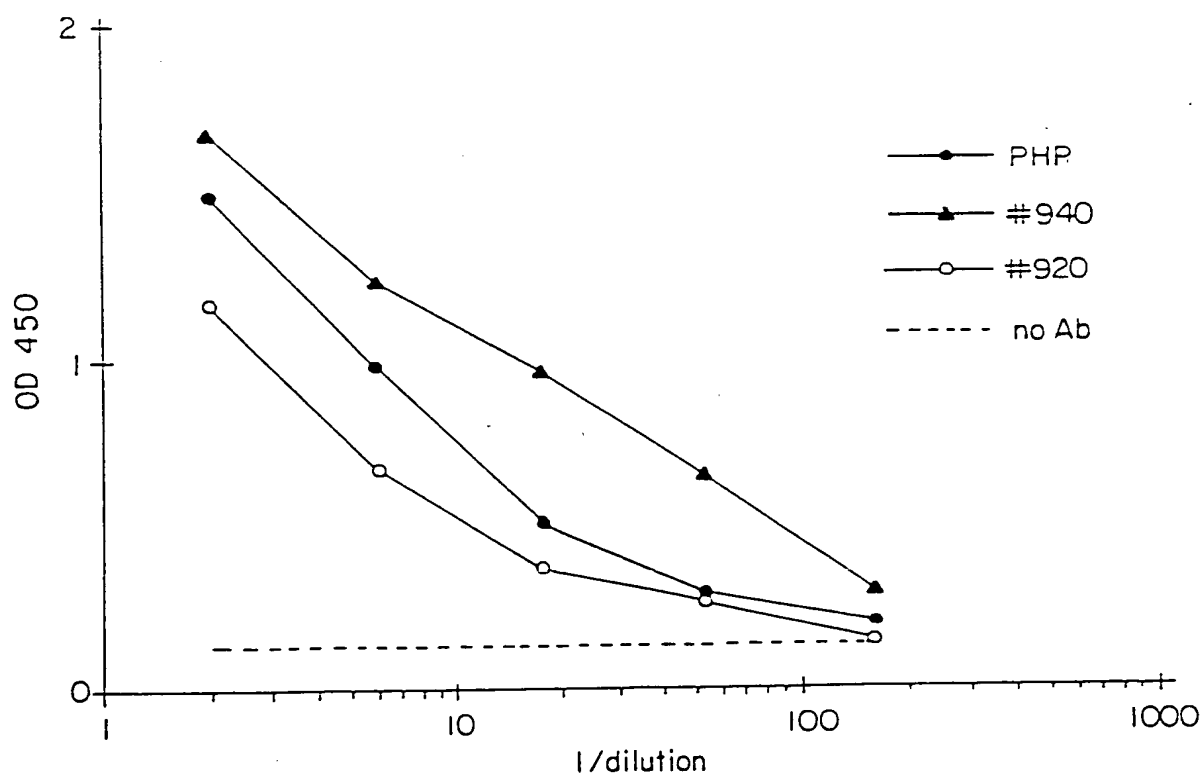


Fig. 5a

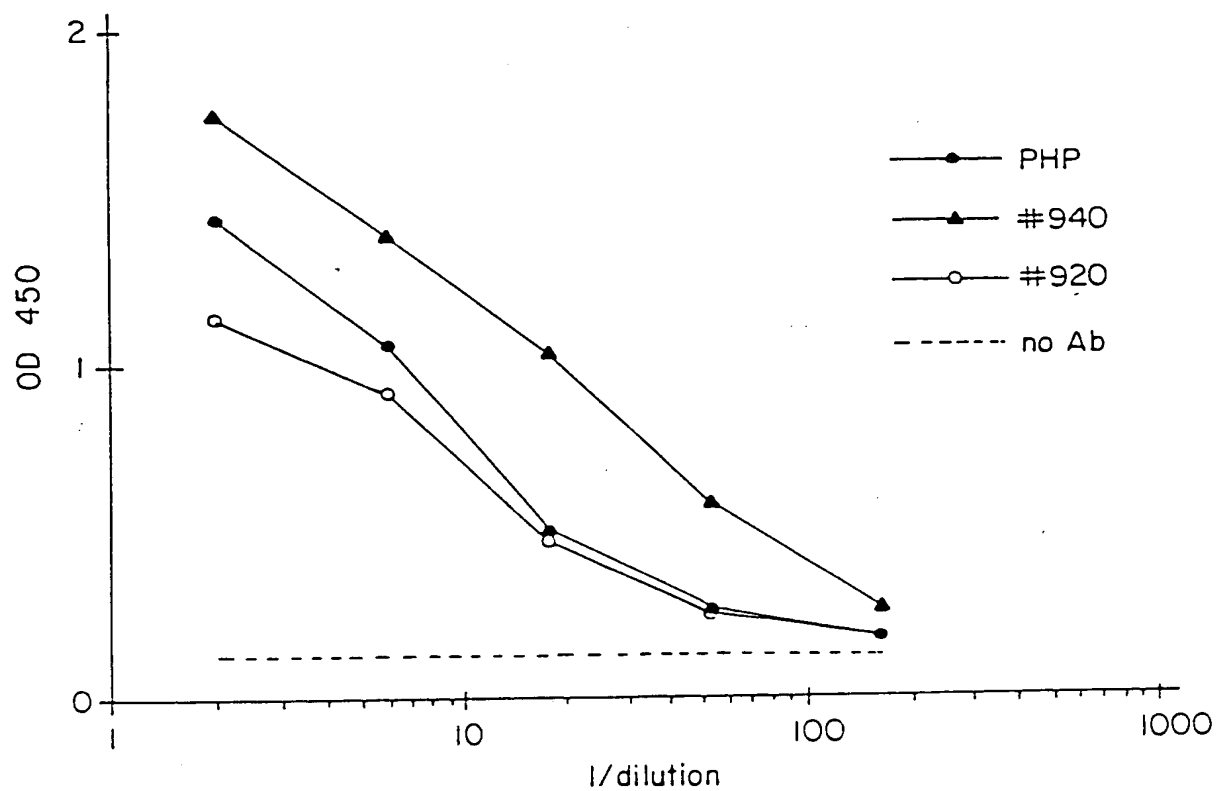


Fig. 5b

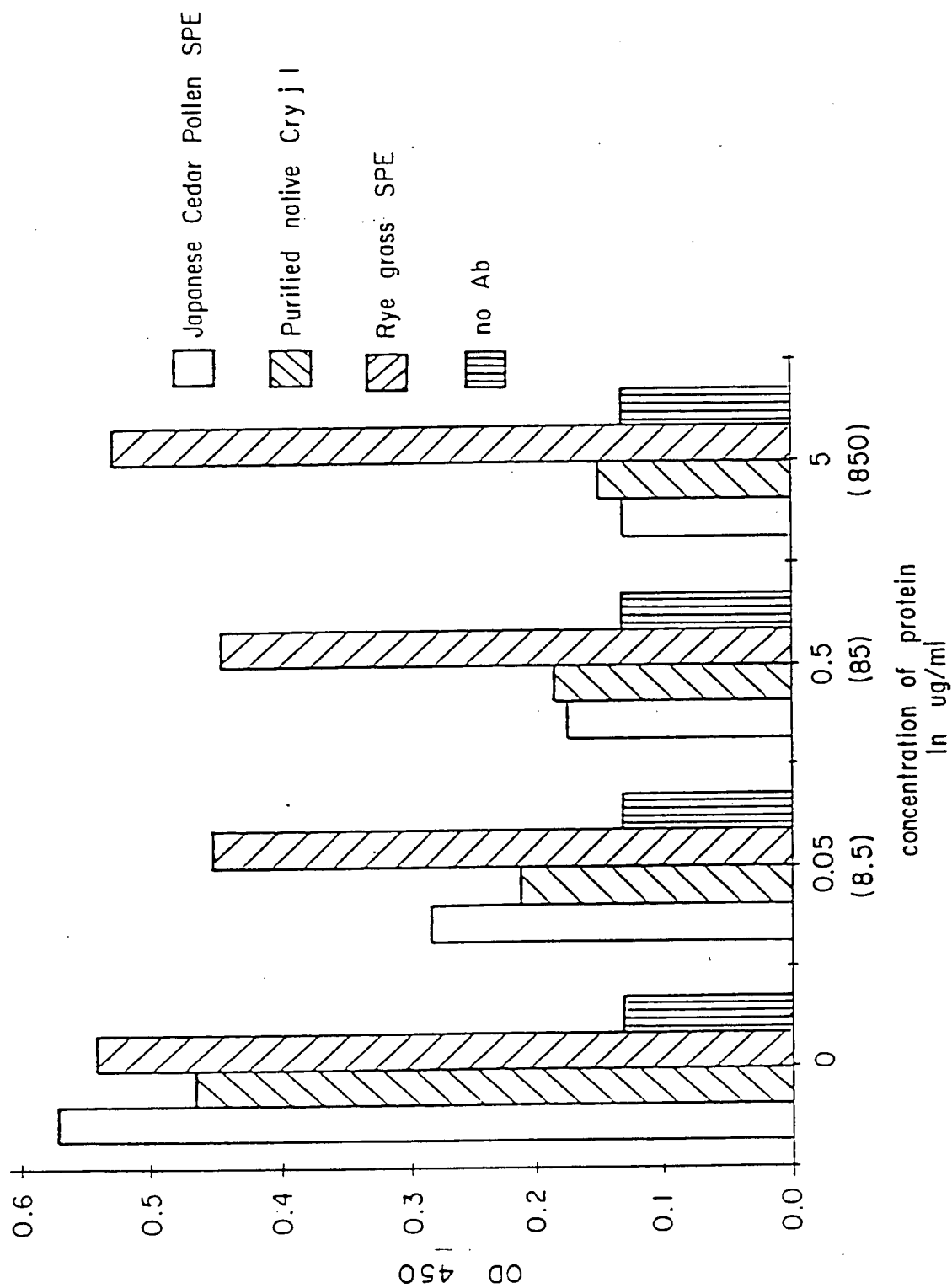


Fig. 6

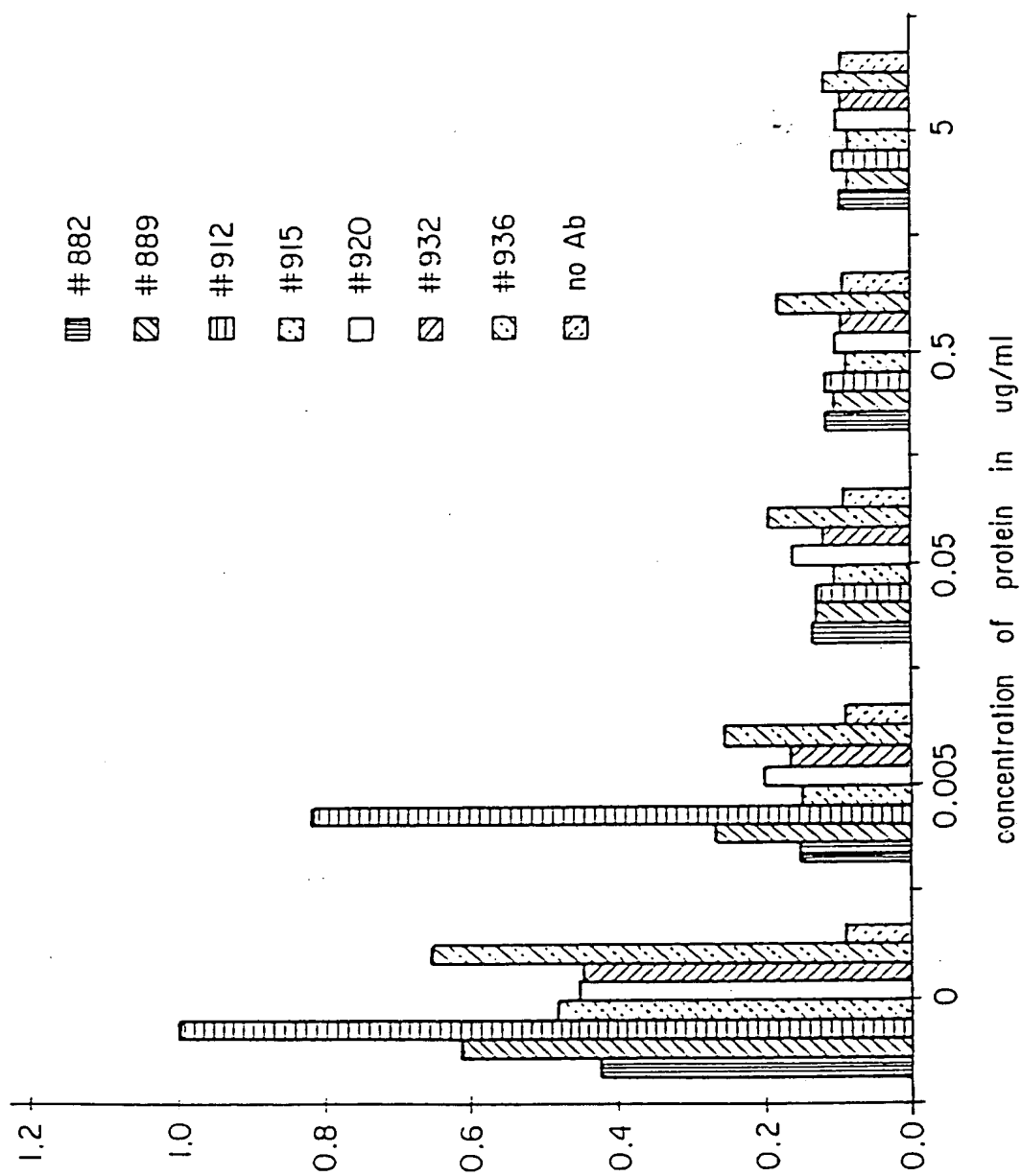


Fig. 7

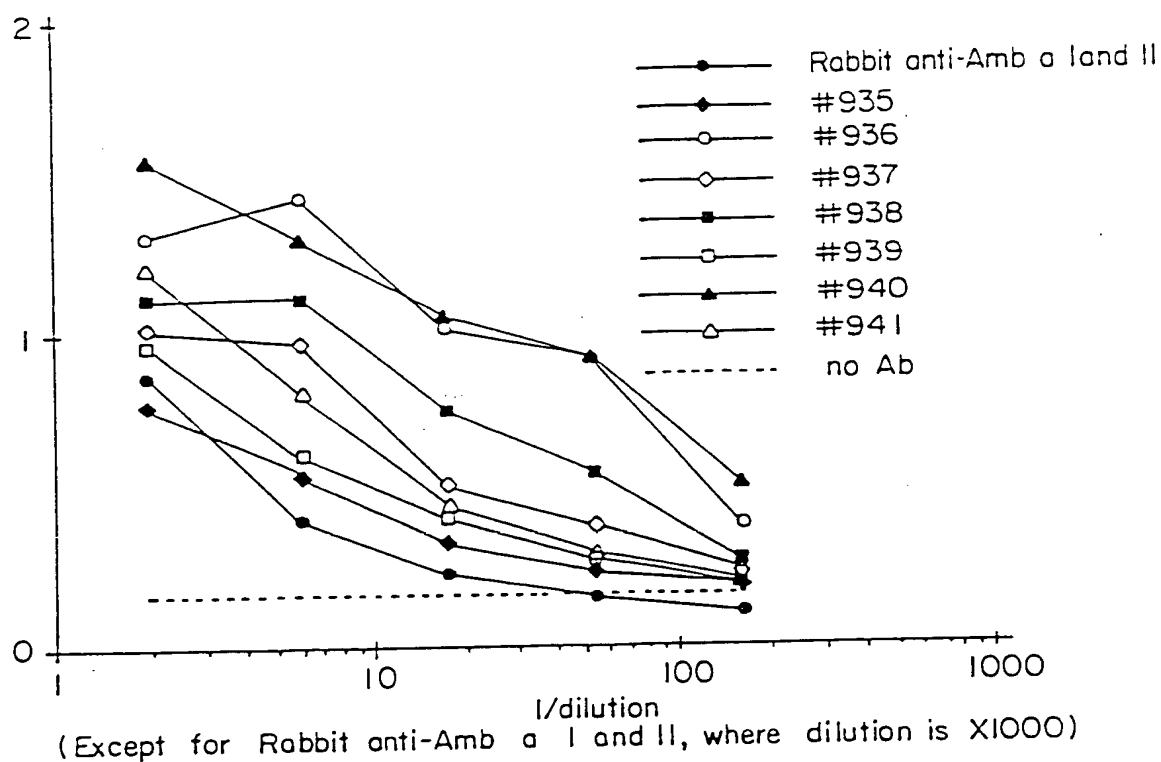


Fig. 8a

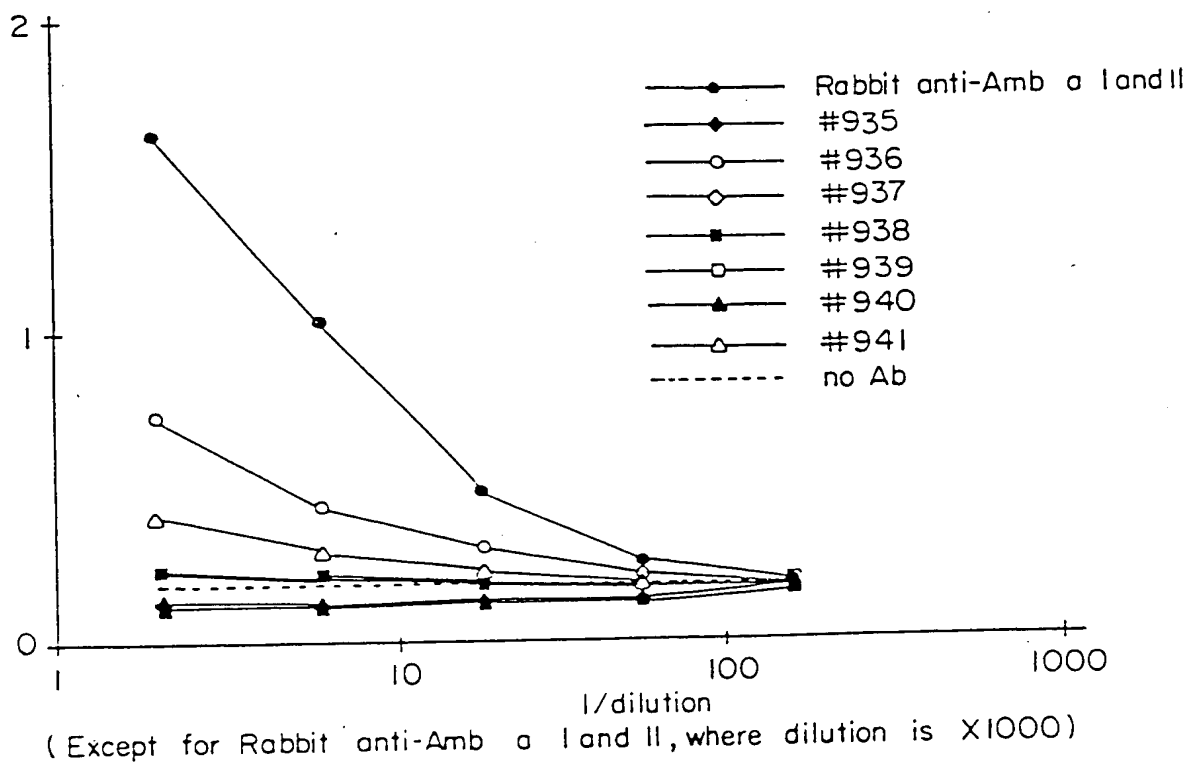
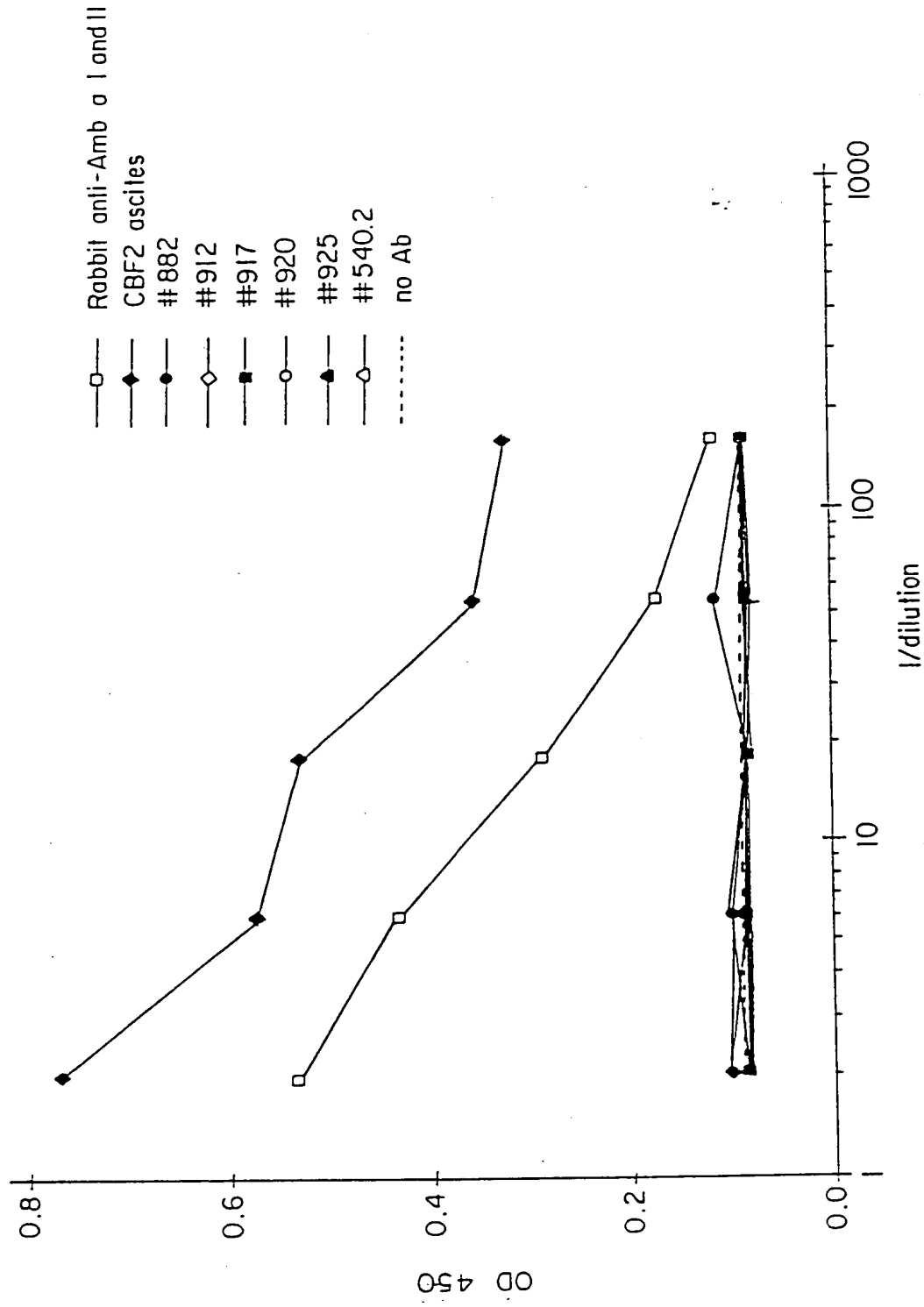


Fig. 8b



(Except for CBF2 and Rabbit anti-Amb α I and II, where dilution is X1000)

Fig. 9

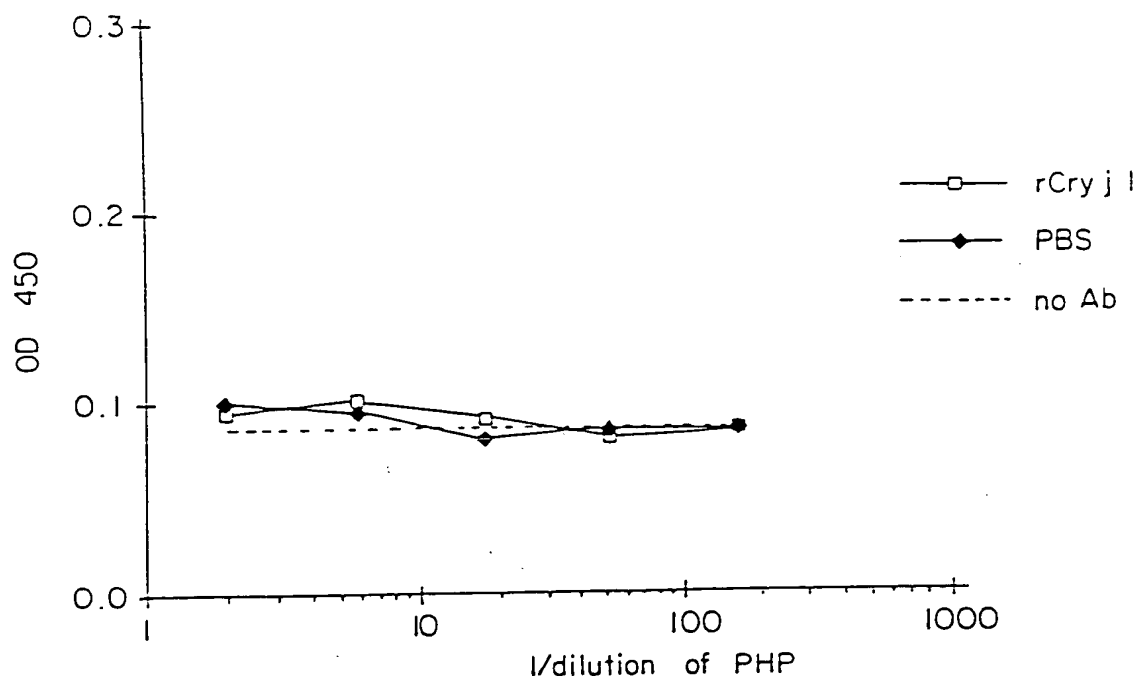


Fig. 10a

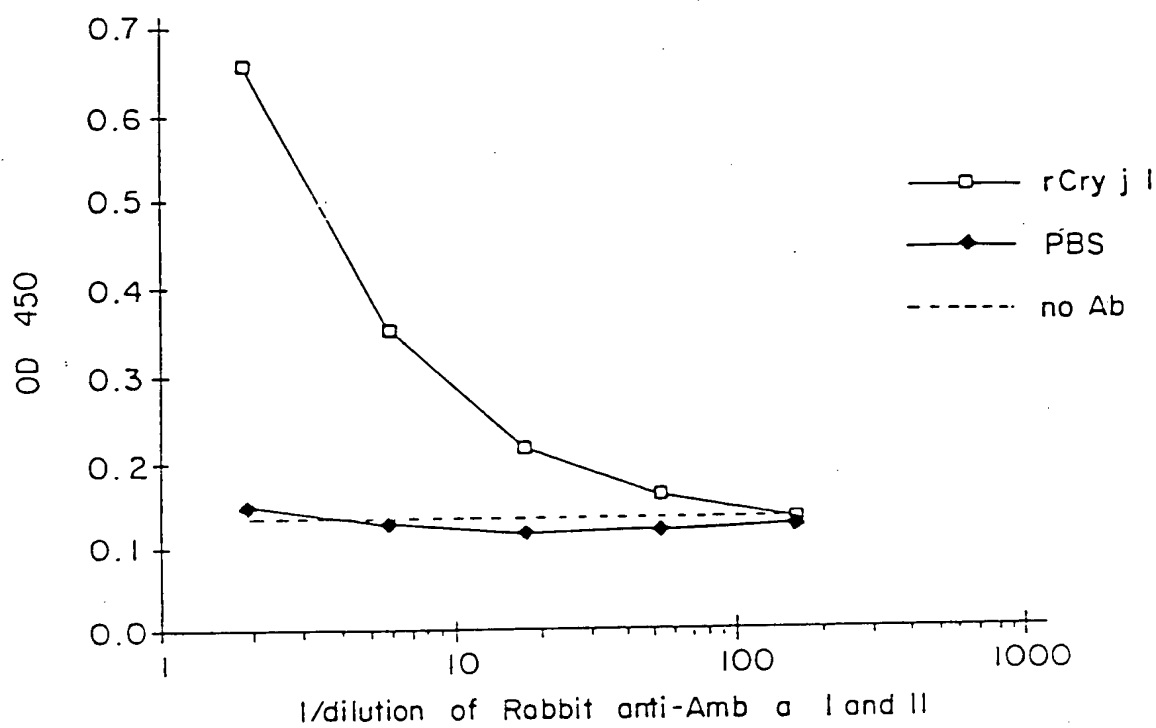


Fig. 10b

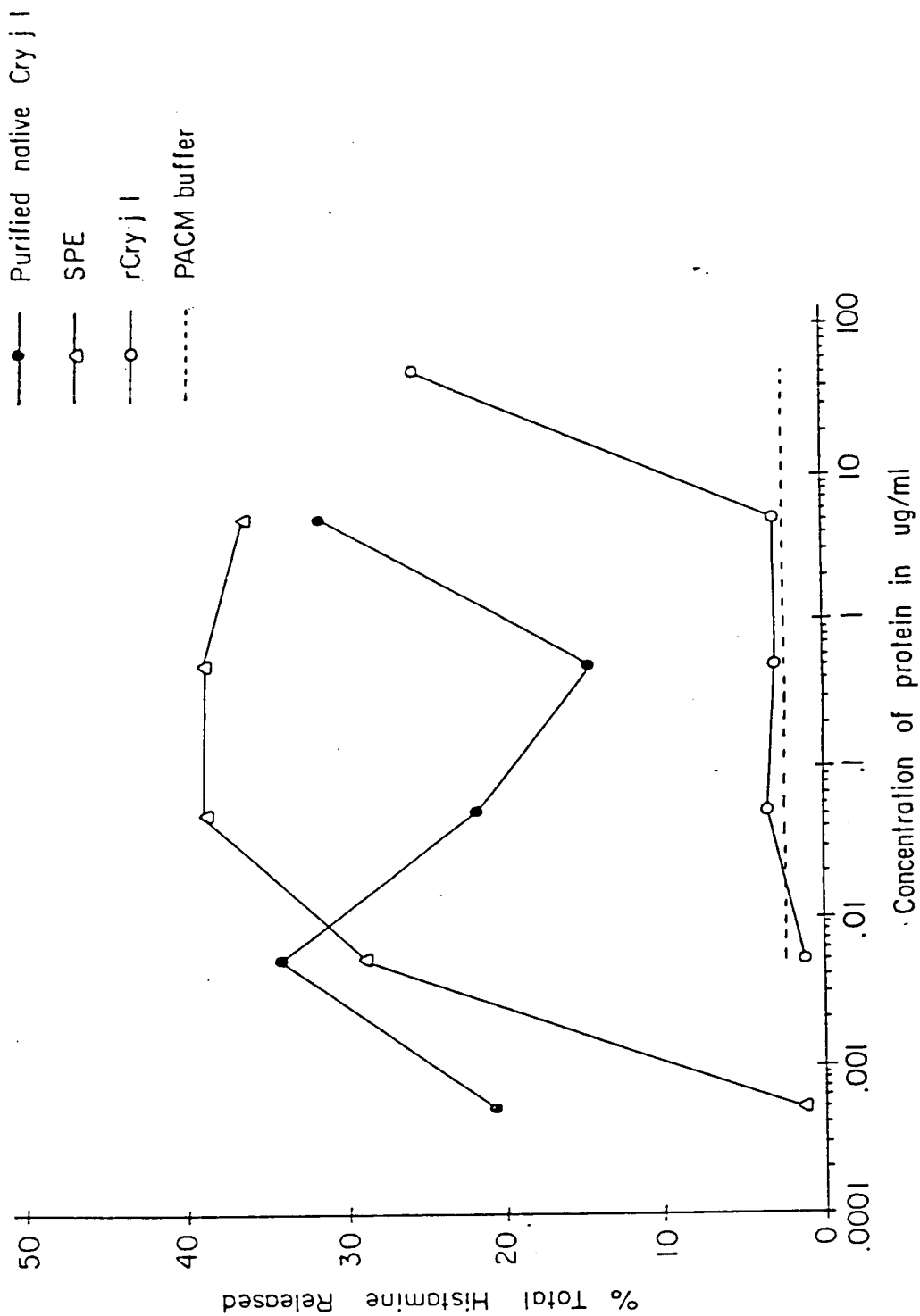


Fig. 11

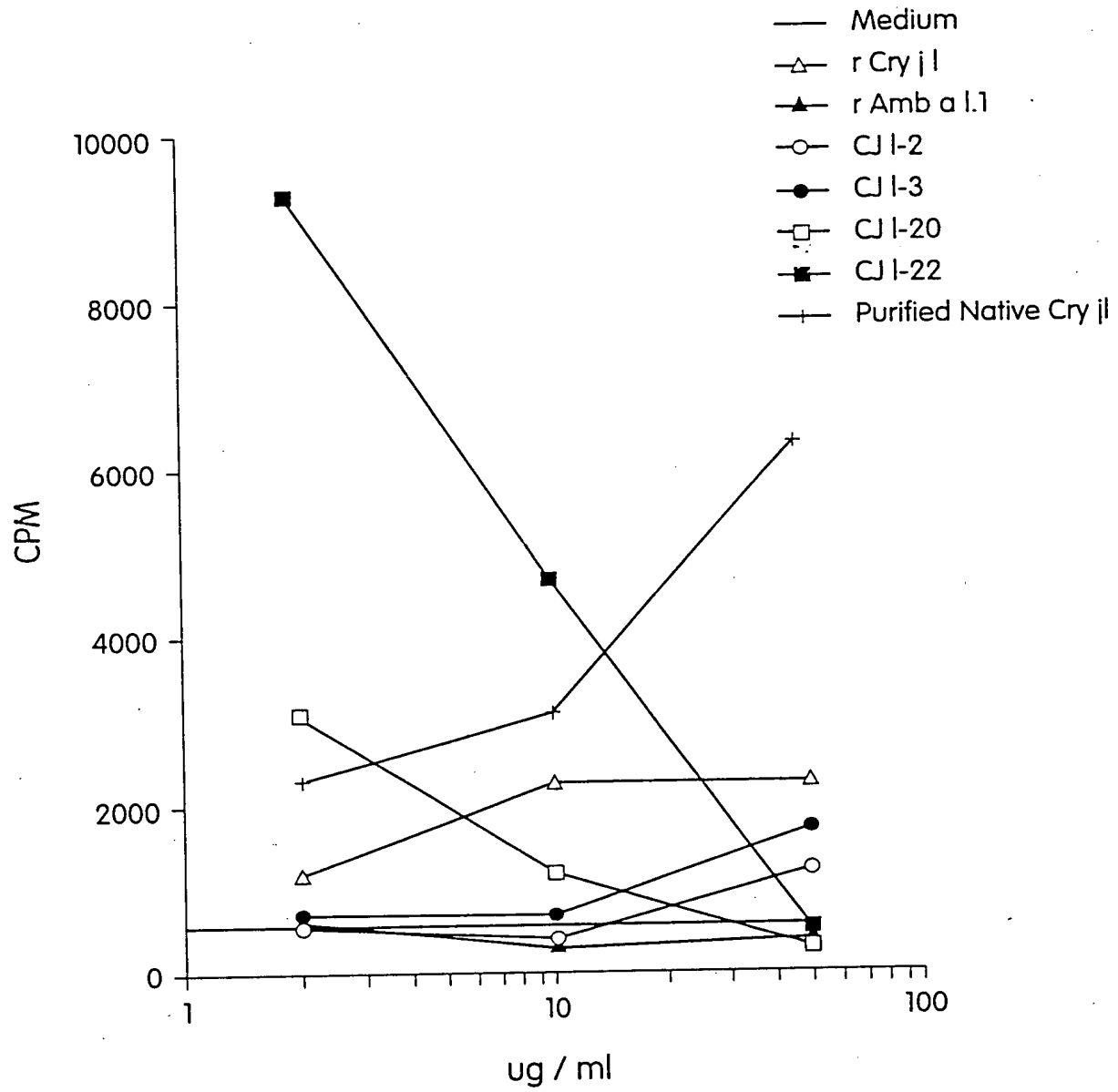


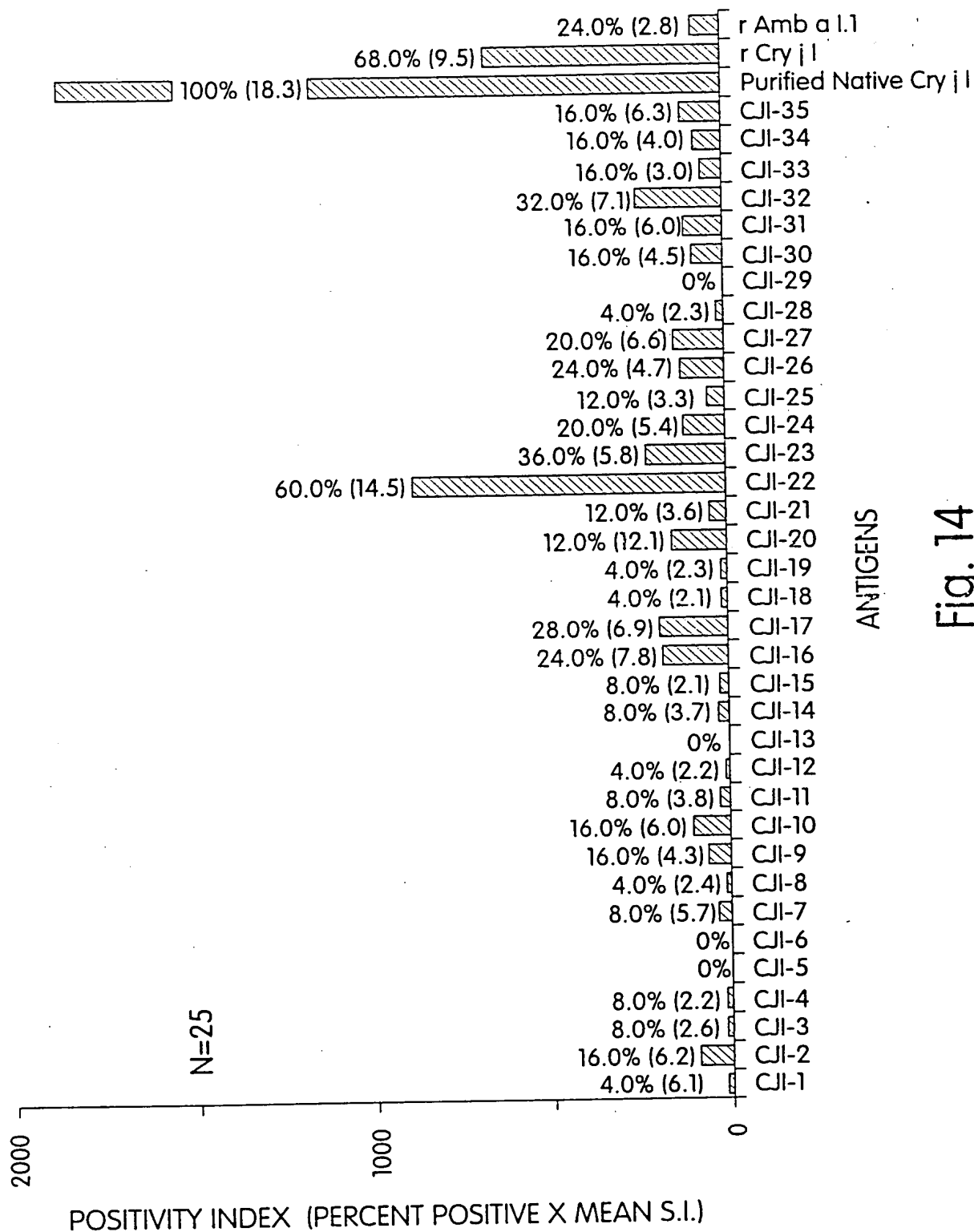
Fig. 12

PEPTIDE NAME

CJI-1 (1-20)
CJI-2 (11-30)
CJI-3 (21-40)
CJI-4 (31-50)
CJI-5 (41-60)
CJI-6 (51-70)
CJI-7 (61-80)
CJI-8 (71-90)
CJI-9 (81-100)
CJI-10 (91-110)
CJI-11 (101-120)
CJI-12 (111-130)
CJI-13 (121-140)
CJI-14 (131-150)
CJI-15 (141-160)
CJI-16 (151-170)
CJI-17 (161-180)
CJI-18 (171-190)
CJI-19 (181-200)
CJI-20 (191-210)
CJI-21 (201-220)
CJI-22 (211-230)
CJI-23 (221-240)
CJI-24 (231-250)
CJI-25 (241-260)
CJI-26 (251-270)
CJI-27 (261-280)
CJI-28 (271-290)
CJI-29 (281-300)
CJI-30 (291-310)
CJI-31 (301-320)
CJI-32 (311-330)
CJI-33 (321-340)
CJI-34 (331-350)
CJI-35 (341-353)

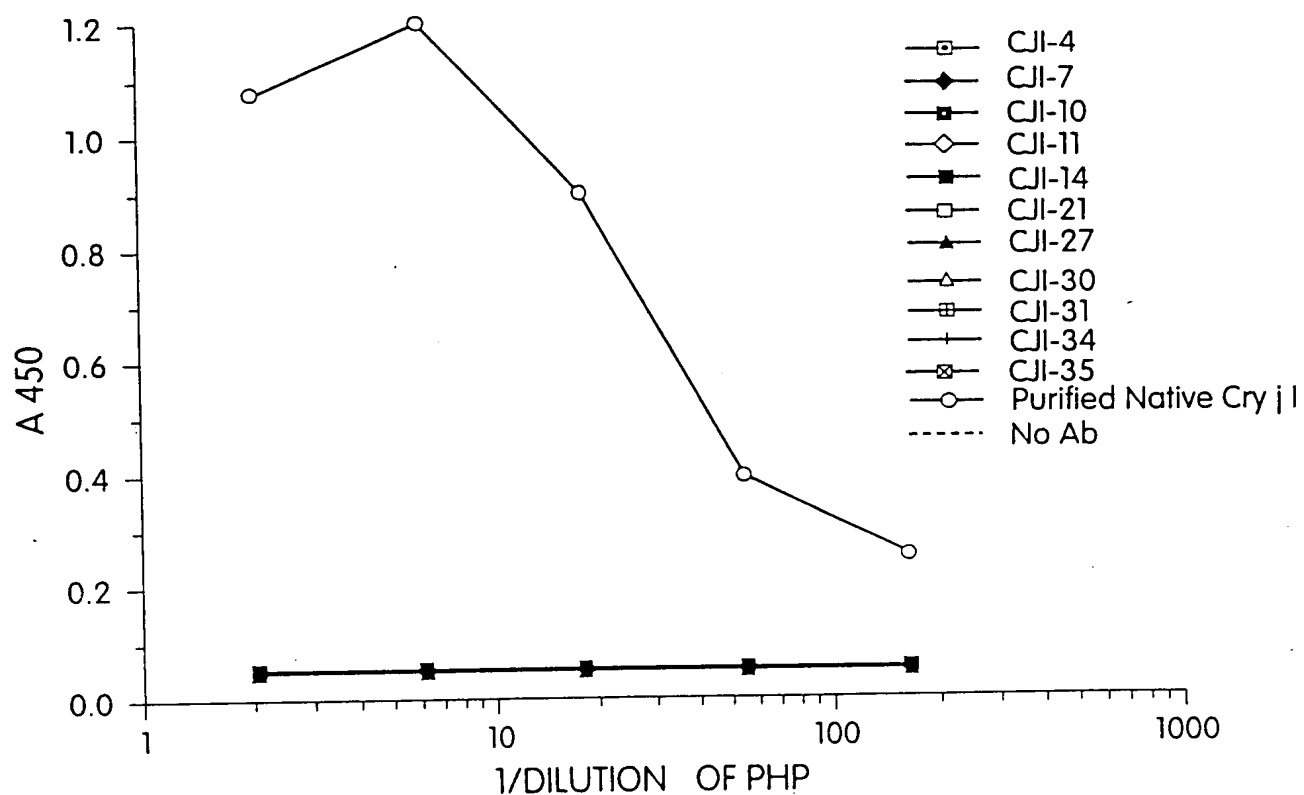
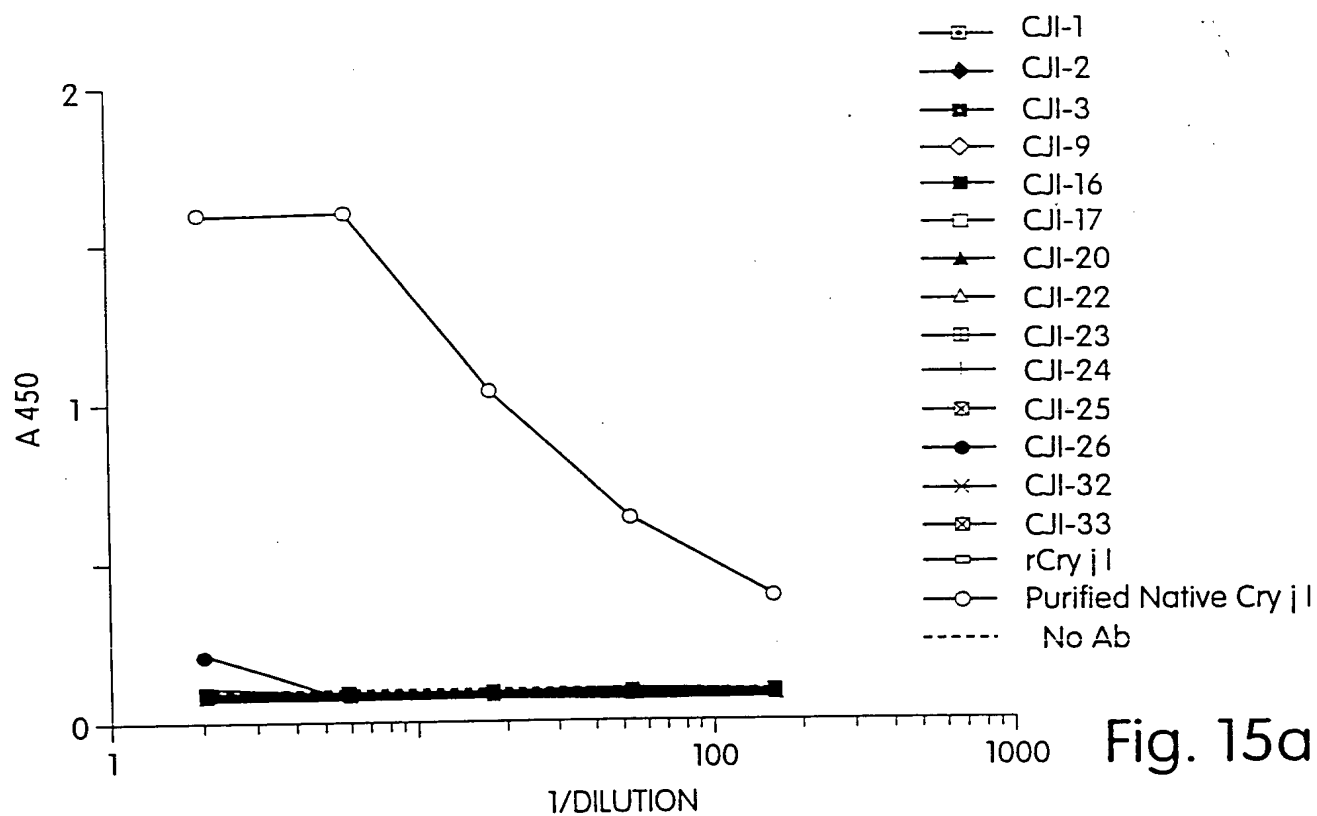
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DSNWAQNRMKLADCAVGFGS
LADCAVGFGSSTMGGKGGDL
STMGGKGGDLYTVTNSDDDP
YTVTNSDDDPVNPAPGTLRY
VNPAPGTLRYGATRDRPLWI
GATRDRPLWIIIFSGNMNIKL
IFSGNMNIKLKMPMYIAGYK
KMPMYIAGYKTFDGRGAQVY
TFDGRGAQVYIGNGGPCVFI
IGNGGPCVFIKRVSNVIIHG
KRVSNVIIHGLYLYGCSTSV
LYLYGCSTSVLGNVLINESEF
LGNVLINESEFGVEPVHPQDG
GVEPVHPQDGDALTTLRTATN
DALTLRTATNIWIDHNSFSN
IWIDHNSFSNSSDGLVDVTL
SSDGLVDVTLTSTGVTISNN
TSTGVTISNNLFFNHHKVML
LFFNHHKVMLLGHDDAYSDD
LGHDDAYSDDKSMKVTVAFN
KSMKVTVAFNQFGPNCGQRM
QFGPNCGQRMPRARYGLVHV
PRARYGLVHVANNNYDPWTI
ANNNYDPWTIYAIGGSSNPT
YAIGGSSNPTILSEGNSFTA
ILSEGNSFTAPNESYKKQVT
PNESYKKQVTIRIGCKTSSS
IRIGCKTSSSCSNWVWQSTQ
CSNWVWQSTQDVFYNGAYFV
DVFYNGAYFVSSGKYEGGNI
SSGKYEGGNIYTKKEAFNVE
YTKKEAFNVENG NATPQLTK
NGNATPQLTKNAGVLTCSLS
NAGVLTCSLSKRC

Fig. 13



ANTIGENS

Fig. 14



5'-AAATTCTATATTCTGAACCCCTAAAAATGGCTTCCCCATGCTTAATAGCAGTCCTTGTTT 60
M A S P C L I A V L V F
-21 -20 -15 -10
CCTTTGTGCAATTGTATCTTGTACTCTGATAATCCCATCGACAGCTGCTGGAGAGAGA 120
L C A I V S C Y S D N P I D S C W R G D
-5 +1 5 10
TTCGAACTGGGATCAAAACAGAAATGAAGCTCGCAGACTGTGCTGGGATTGGGAAGCTC 180
S N W D Q N R M K L A D C A V G F G S S
15 20 25 30
CACCATGGGAGGCAAAAGGAGGAGATTTTACACCGTCACAAGCACAGATGATAATCCTGT 240
T M G G K G G D F Y T V T S T D D N P V
35 40 45 50
GAATCCCTACACCAGGAACTTTGGCGCTATGGAGCAACAAGAGAAAAGCAGCTTTGGATCAT 300
N P T P G T L R Y G A T R E K A L W I I
55 60 65 70
TTTCTCTCAGAATATGAATATAAAGCTCAAGATGCCCTTTGTATGTGCTGGACATAAGAC 360
F S Q N M N I K L K M P L Y V A G H K T
75 80 85 90
TATTGACGGCAGGGAGCAGATGTTTCATCTTGGCAACGGCGGTCCCTGTCTGTTTATGAG 420
I D G R G A D V H L G N G G P C L F M R
95 100 105 110

Fig. 16

GAAAGTGAGCCATGTTATTCTCCATAGTTTGCAATATACACGGTTGTAATACGAGTGTTT 480
K V S H V I L H S L H I H G C N T S V L
115 120 125 130

GGGGGATGTTTGGTAAGTGAGTCTATTGGGGTCGAGCCTGTTTCATGCTCAGGATGGGGA 540
G D V L V S E S I G V E P V H A Q D G D
135 140 145 150

CGCCATTAATGCGCCATGTTACAAATGCTTGGATTGATCATAAATTCCTCTCCGATG 600
A I T M R H V T N A W I D H N S L S D C
155 160 165 170

TTCTGATGGTCTTATCGATGTTACGCTTGGCTCCACTGGAATTACTATCTCCAACAATCA 660
S D G L I D V T L G S T G I T I S N N H
175 180 185 190

CTTCTTCAACCATCATAAAGTGATGTTATTAGGACATGATGATACATATGACGATGACAA 720
F F N H H K V M L L G H D D T Y D D K
195 200 205 210

ATCTATGAAAGTGACAGTGGCGTTCAATCAATTGGACCTAATGCTGGGCAAGAATGCC 780
S M K V T V A F N Q F G P N A G Q R M P
215 220 225 230

Fig. 16 cont.

AAGGCACGATATGGACTTGTACATGTTGCAACAATAATTATGATCCATGGAAATATATA 840
R A R Y G L V H V A N N Y D P W N I Y
235 240 245 250

TGCTATTGGTGGGAGTTCAAATCCAACCAATTCTGAGTGAAGGGAATAGTTTCACTGCCCC 900
A I G G S S N P T I L S E G N S F T A P
255 260 265 270

AAGTGAGAGTTACAAGAAGCAAGTAACAAGCGTATAGGGTGTGAATCACCATCAGCTTG 960
S E S Y K K Q V T K R I G C E S P S A C
275 280 285 290

TGCGAACTGGGTGGAGATCTACACGAGATGCTTTTATTAATGGAGCTTATTTGTATC 1020
A N W V W R S T R D A F I N G A Y F V S
295 300 305 310

ATCGGGGAAACTGAAGAGACCAATATATACAATAGTAATGAAGCTTTCAAAAGTTGAGAA 1080
S G K T E E T N I Y N S N E A F K V E N
315 320 325 330

TGGGAATGCAGCTCCTCAATTAACCAAAAATGCTGGAGTTGTAACTAAGCTCTCTCTAA 1140
G N A A P Q L T K N A G V V T -
335 340 345

ATCTTGCTTATGAAACGAAAAAATATATAG-3' 1170

Fig. 16 cont.

'-CGGTATAGATTTCTATATTCTGAGCCCTAAAAATGGCTTCCCCATGCTTAATAGCAT 60

M A S P C L I A

-21 -20 -15

TCCTTGTTCCTTTGTGCAATTGTATCTTTGTTGCTCTGTGATAATCCCATAGACAGCTGCT 120

F L V F L C A I V S C C S D N P I D S C

-10 -5 +1 5

GGAGAGGAGATTCGAACTGGGGTCAAAACAGAAATGAAGCTCGCAGATTGCGCTGTGGGAT 180

W R G D S N W G Q N R M K L A D C A V G

10 15 20 25

TTGGAAAGCTCCACCATGGGAGGCAAAAGGAGGAGATTTTACACCGTCACAAGCGCAGATG 240

F G S S T M G G K G G D F Y T V T S A D

30 35 40 45

ATAATCCTGTGAATCCTACACCAGGAACTTTGCGCTATGGAGCAACAAGAGAAAAAGCAC 300

D N P V N P T P G T L R Y G A T R E K A

50 55 60 65

TTTGGAATCATTTCTCTCAGAAATATGAATATAAAGCTCAAGATGCCCTTTGTATGTTGCTG 360

L W I I F S Q N M N I K L K M P L Y V A

70 75 80 85

GACATAAGACTATTGACGGCAGGGGAGCAGATGTTTCATCTTGGCAACGGCGGTCCTGTC 420

G H K T I D G R G A D V H L G N G G P C

90 95 100 105

Fig. 17

08/226248

TGTTTATGAGGAAAGTGAGCCATGTTATTCTCCATGGTTTGCCATATACACGGTTGTAATA 480
 L F M R K V S H V I L H G L H I H G C N
 110 115 120 125

 CTAGTGTTTTGGGGGATGTTTGGTAAGTGAGTCTATTGGGGTGGTGCCGTGACACCCCC 540
 T S V L G D V L V S E S I G V V P V H P
 130 135 140 145

 AGGACGGAGATGCGTTTACTGTGAGGACCTCTGAACATATTGGGTCGACCAATAACTC 600
 Q D G D A F T V R T S E H I W V D H N T
 150 155 160 165

 TCTCCAATGGCACCGACGGCCTCGTCGACGTTACTCTTGCTTCCACTGCTGTACTATT 660
 L S N G T D G L V D V T L A S T A V T I
 170 175 180 185

 CCAATAACCACCTTCTCGACCATGATGAAGTGATGTTGTTAGGACATAGTGATTCAATTCT 720
 S N N H F F D H D E V M L L G H S D S F
 190 195 200 205

 CAGATGATAAAGTGATGAAAGTCACAGTTGCATTTAACCACCTTTGGACCTAATTGTGTGC 780
 S D D K V M K V T V A F N H F G P N C V
 210 215 220 225

 AACGATGCCAAGGGCTAGATATGGACACTTTCATGTTGTTAAATAATATGAGCCAT 840
 Q R L P R A R Y G H F H V V N N N Y E P
 230 235 240 245

Fig. 17 cont.

GGGAAATATGCCATTGGAGGAAGTTCTGATCCAACAATTATAAGTGAAGGAATAGAT 900

W G K Y A I G G S S D P T I I S E G N R
250 255 260 265

TTCTTGCAACCAATGAATCTTATAAAAGGAGGTGACAATACGTGTAGTTGTAATCTA 960

F L A P N E S Y K K E V T I R V G C K S
270 275 280 285

CAAGTTGTGATGCGAGTGGAGATCAAAAGATGATGCCCTTCTTAATGGTGCCTATT 1020

T S C D A W E W R S K D D A F L N G A Y
290 295 300 305

TTGTACAATCAGGCAAGGGGTATAATGGTGGAGAGGCATTCAAGGTTGAAAGTGCAAATG 1080

F V Q S G K G Y N G G E A F K V E S A N
310 315 320 325

AGGTGCCAACATTGACTAAACATGCTGGAGCATTAATAATGTATACCTACCAACAATGTG 1140

E V P T L T K H A G A L K C I P T K Q C
330 335 340 345

TGATATGAAAAGTCAATCGATATAATAATGTGTTATTTGTAATATTTTCAGCTTTGAATAT 1200

V I -

GTATAGAAAAGAATTCAACAAAATGACACTATTATATAAAATAAATCTTAGTTTATTA 1260

GTGGGTATTAATAAAAAA-3' 1278

Fig. 17 cont.

CJI-41 KMPMYIAGYKTFDGRGAQVYIGNGGPCVFI
CJI-41.1 PMYIAGYKTFDGRGAQVYIGNGGP
CJI-41.2 YIAGYKTFDGRGAQVYIGNGGP
CJI-41.3 KKYIAGYKTFDGRGAQVYIGNGGP

CJI-42 DALTLRTATNIWIDHNSFSNSSDGLVDVTL
CJI-42.1 RTATNIWIDHNSFSNSSDGLVD
CJI-42.2 KRTATNIWIDHNSFSNSSDGLVDK

CJI-43 KSMKVTVAFNQFGPNCGQRMPRARYGLVHVANNYD
CJI-43.1 KSMKVTVAFNQFGPNCGQRMPRARYGLVHV
CJI-43.6 KSMKVTVAFNQFGPNSGQRMPRARYGLVHV
CJI-43.7 KSMKVTVAFNQFGPNCGQRMPRARYGLV
CJI-43.8 KSMKVTVAFNQFGPNSGQRMPRARYGLV
CJI-43.9 KSMKVTVAFNQFGPNCGQRMPRARYG
CJI-43.10 KSMKVTVAFNQFGPNSGQRMPRARYG
CJI-43.11 KSMKVTVAFNQFGPNSGQRMPRARYGKK
CJI-43.12 KSMKVTVAFNQFGPNCGQRMPRARYG

CJI-45 PRARYGLVHVANNYDPWTIYAIGGSSNPT
CJI-45.1 RARYGLVHVANNYDPWTIYAIGGSSNP
CJI-45.2 RARYGLVHVANNYDPWTIYAIGGSS

CJI-44 DVFYNGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.1 NGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.2 NGAYFVSSGKYEGGNIYTKKEAFN
CJI-44.3 KKNLAYFVSSGKYEGGNIYTKKEAFN

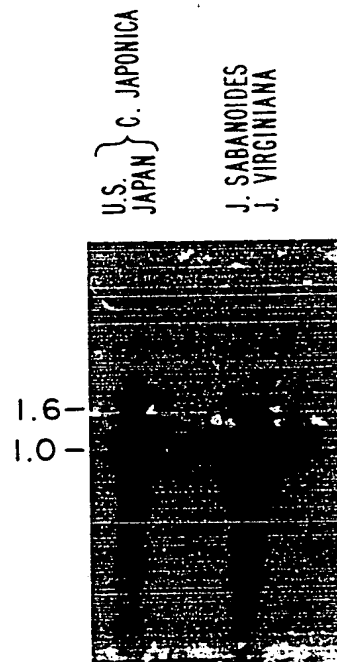
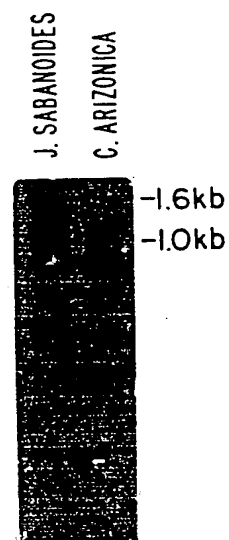
*Fig. 19a**Fig. 19b*

Fig. 20

CJI-42.5 DERTATNIWIDHNSFSNSSDD
CJI-42.8 DERTATNIWIDHNSFSNSSDGLAD

CJI-43.26 DEKSMKATVAFNQFGPNDE
CJI-43.27 DEKSMKVTA AFNQFGPNDE
CJI-43.30 DEEKSMKATVAFNEFGPNDEE
CJI-43.31 DEEKSMKVTV AANQFGPNDEE
CJI-43.32 DEEKSMKVTVAFNQAGPNDEE
CJI-43.35 DEKSMKATAAFNQFGPNDE
CJI-43.36 DEEKSMKATAAFNQFGPNDEE
CJI-43.39 DDAYSDDKSMKVTVAFNQFGDE

CJI-24.5 DKEPRARYGLVHVANN NYDPWTIEEE

CJI-44.5 DENGAYFVSSGKYEGGNIYTKKEAFNAE
CJI-44.6 DEENGAYFVSSGKYEGGNIYTKKEAFNVE
CJI-44.8 DEEGAYFVSSGKYEGGNIYTKKEAFNVE

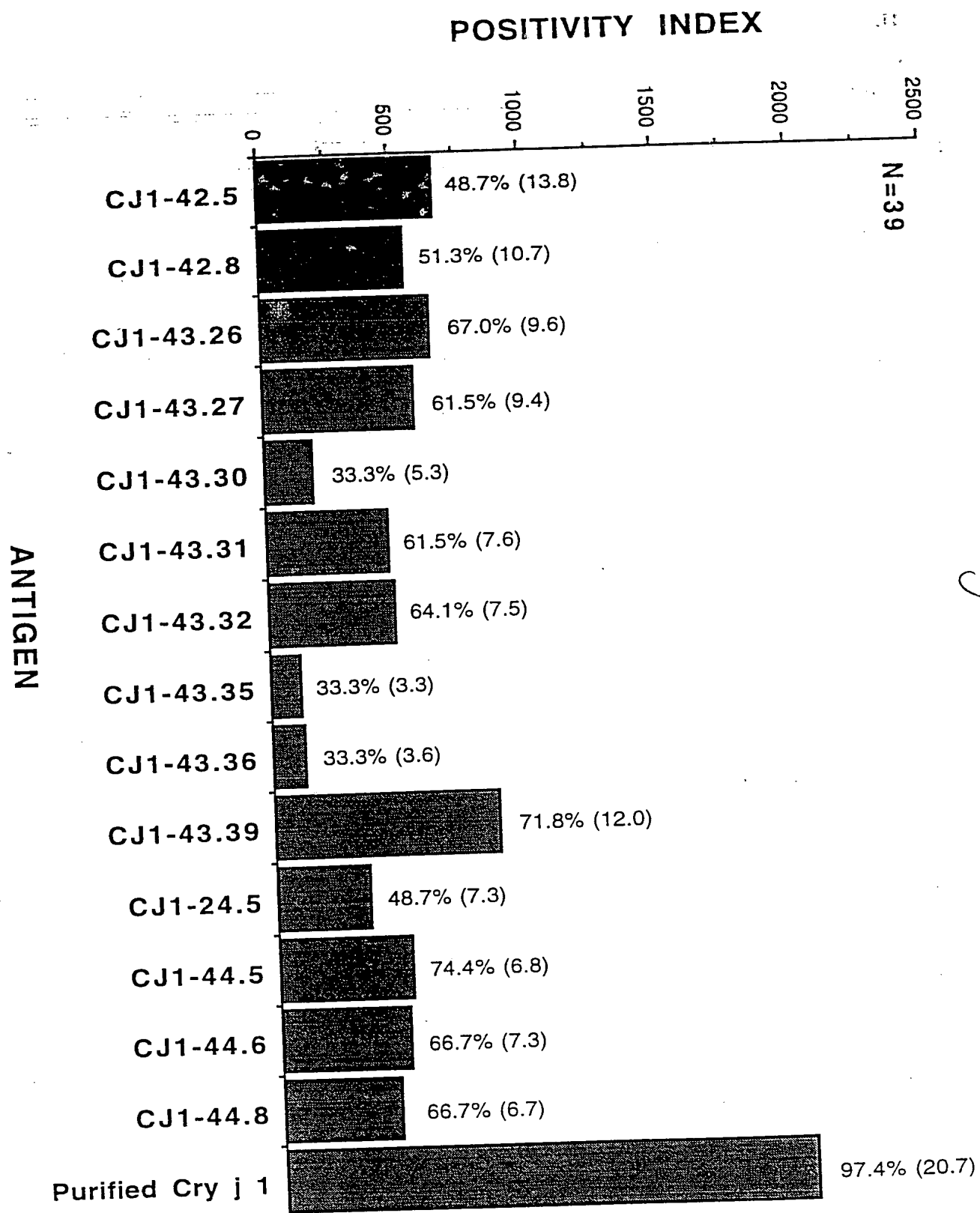
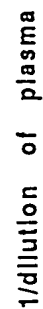
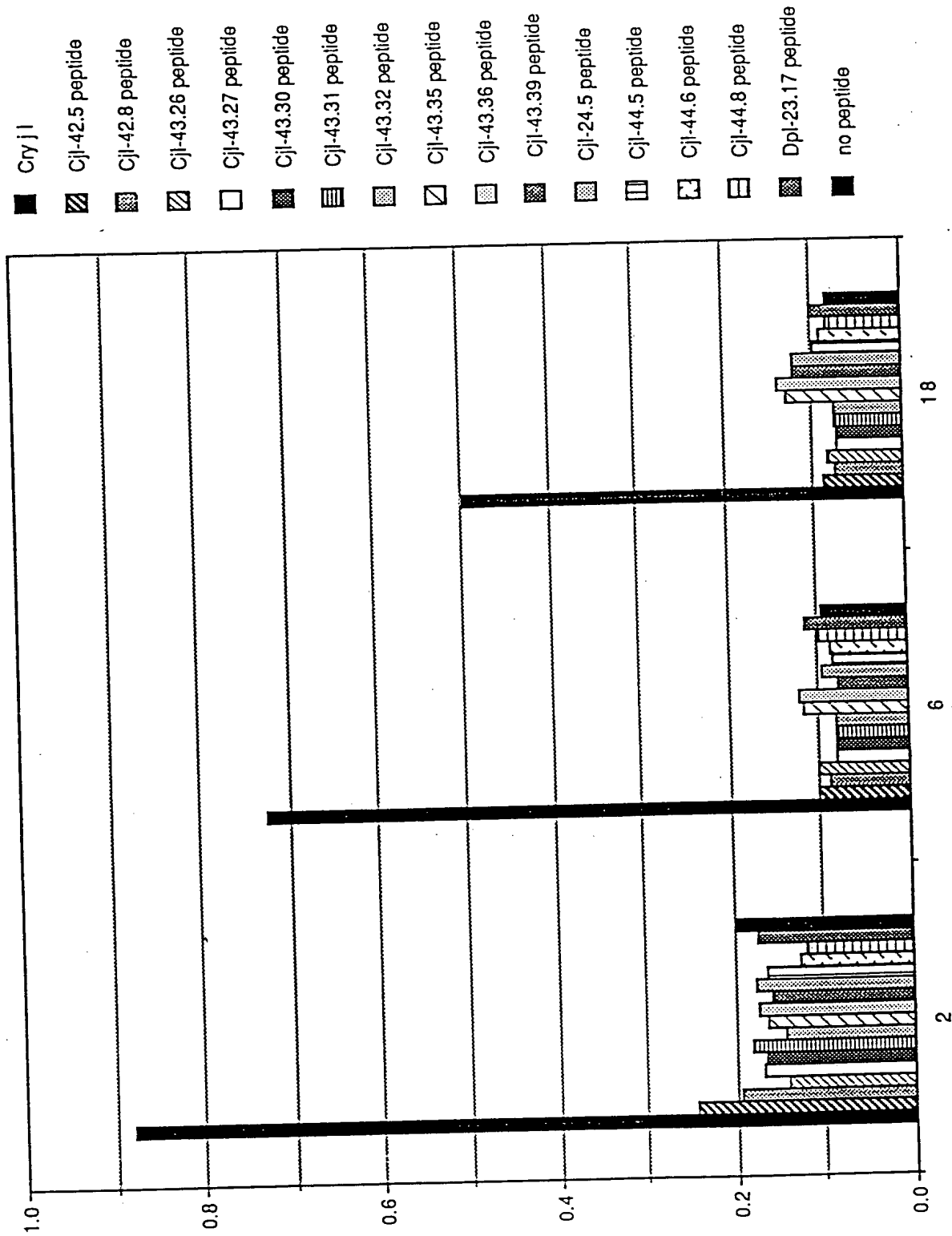


Fig. 21





1/dilution of plasma

Fig. 23

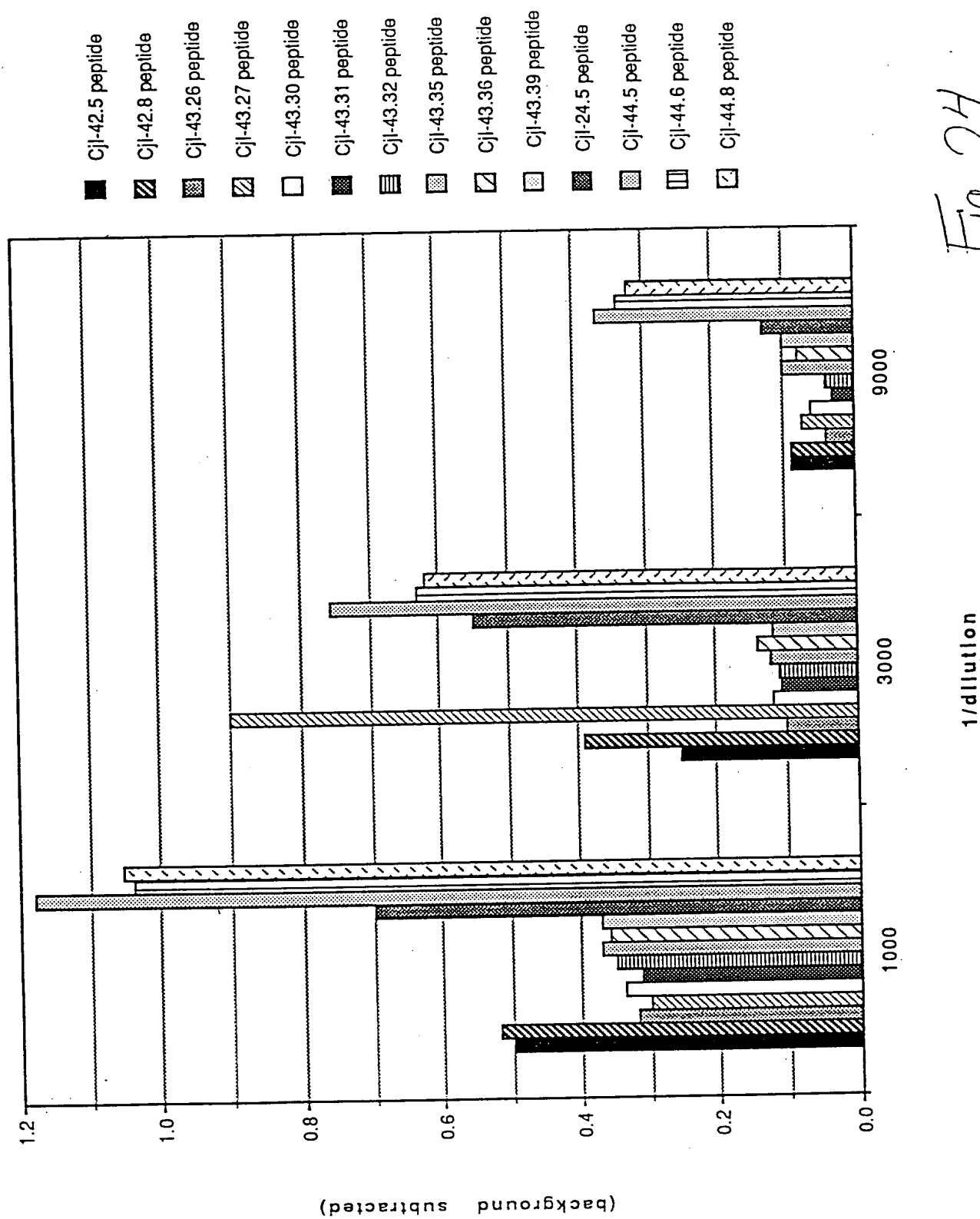


Fig. 24

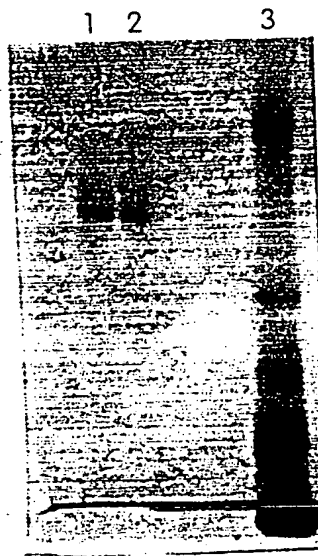


Fig. 25a

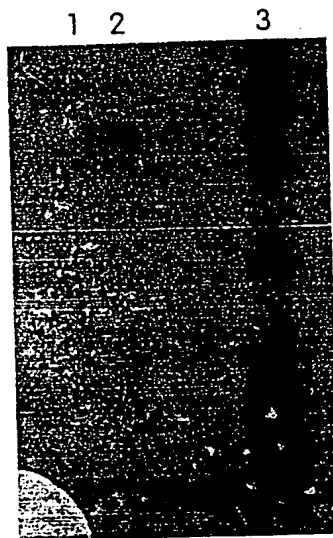


Fig. 25b

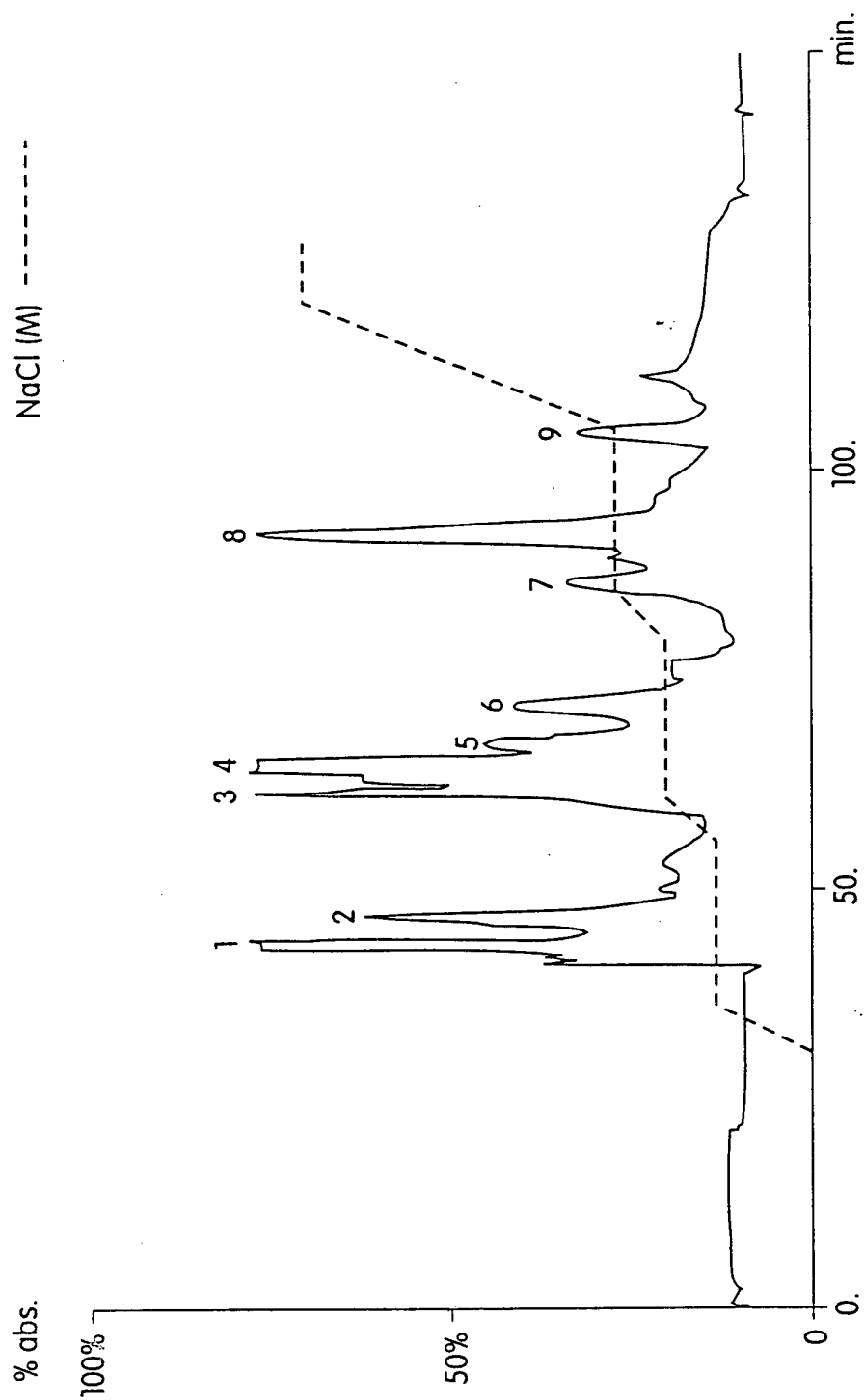


Fig. 26

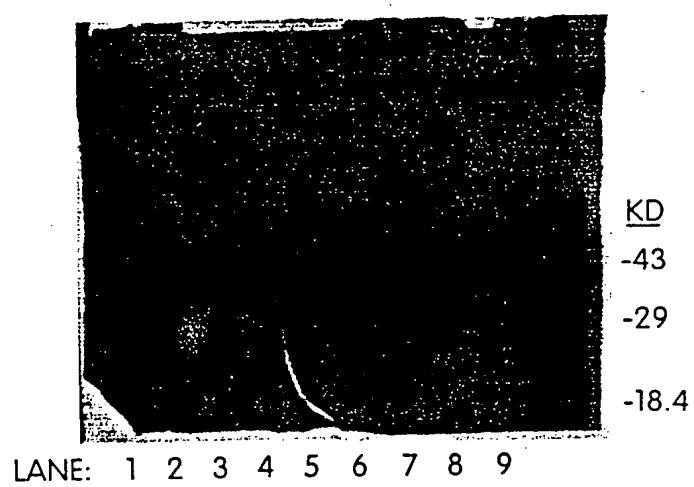


Fig. 27

10 20 30 40 50 60
 | | | | |
 TGAGTTCGAGACAAGTATAGAAAGAATTTCTTTTATTAATAATGGCCATGAAATTAATTG
 M A M K L I

70 80 90 100 110 120
 | | | | |
 CTCCAATGGCCCTTCTGGCCATGCAATGATTAATAATGGCGGCAGCAGAAGATCAATCTG
 A P M A F L A M Q L I I M A A A E D Q S
 10 20

130 140 150 160 170 180
 | | | | |
 CCCAAATATGTTGGACAGTGTGTGTCGAAAAATATCTTAGATCGAATCGGAGTTTAAGAA
 A Q I M L D S V V E K Y L R S N R S L R
 30 40

190 200 210 220 230 240
 | | | | |
 AAGTTGAGCATTCGTCATGATGCTATCAACATCTTCAATGTGGAAGTATGGCGCAG
 K V E H S R H D A I N I F N V E K Y G A
 50 60

Fig. 28

250 | 260 | 270 | 280 | 290 | 300 |
 TAGGCGATGGAAGCATGATTGCACTGAGGCATTTCAACAGCATGGCAAGCTGCATGCA
 V G D G K H D C T E A F S T A W Q A A C
 70 80
 310 | 320 | 330 | 340 | 350 | 360 |
 AAAACCCATCAGCAATGTTGCTTGTCAGGCAGCAAGAAATTTGTGTAAACAATCTGT
 K N P S A M L L V P G S K K F V V N N L
 90 100
 370 | 380 | 390 | 400 | 410 | 420 |
 TCTTCAATGGGCCATGTCAACCTCACTTTACTTTAAGGTAGATGGGATAATAGCTGCCGT
 F F N G P C Q P H F T F K V D G I I A A
 110 120
 430 | 440 | 450 | 460 | 470 | 480 |
 ACCAAAATCCAGCGAGCTGGAAGAATAATAGAATATGGTTGCAGTTTGCTAAACTTACAG
 Y Q N P A S W K N N R I W L Q F A K L T
 130 140

Fig. 28 Cont.

```

490      |      500      |      510      |      520      |      530      |      540      |
      |      |      |      |      |      |      |
GTTTACTCTAATGGGTAAGGTGTAATTGATGGGCAAGGAAACAATAATGGTGGCTGGCC
G F T L M G K G V I D G Q G K Q W A G
150
550      |      560      |      570      |      580      |      590      |      600      |
      |      |      |      |      |      |      |
AATGTAATGGGTCAATGGACGAGAAATTTCGAACGATCGTGATAGACCAACAGCCATTA
Q C K W V N G R E I C N D R D R P T A I
170
610      |      620      |      630      |      640      |      650      |      660      |
      |      |      |      |      |      |      |
AATTCGATTTTCCACGGGTCTGATAATCCAAGGACTGAAACTAATGAACAGTCCCGAAT
K F D F S T G L I I Q G L K L M N S P E
190
670      |      680      |      690      |      700      |      710      |      720      |
      |      |      |      |      |      |      |
TTCATTTAGTTTGGGAATTGTGAGGAGTAAATAATCATCGGCATTAGTATTACGGCAC
F H L V F G N C E G V K I I G I S I T A
210

```

Fig. 28 Cont.

730 | 740 750 760 770 780
 CGAGAGACAGTCCTAACACTGATGGAATTGATATCTTTGCATCTAAAACTTTCACCTAC
 P R D S P N T D G I D I F A S K N F H L
 230 240

790 | 800 810 820 830 840
 AAAAGAACACGATAGGAACAGGGGATGACTGCCGTCGCTATAGGCACAGGGTCTTCTAATA
 Q K N T I G T G D D C V A I G T G S S N
 250 260

850 | 860 870 880 890 900
 TTGTGATTGAGGATCTGATTTGCCGGTCCAGGCCATGGAATAAGTATAGGAAGTCTTGGGA
 I V I E D L I C G P G H G I S I G S L G
 270 280

910 | 920 930 940 950 960
 GGGAAACTCTAGAGCAGAGGTTTCATACGTGCACGTAATGGGGCTAAATTCATAGACA
 R E N S R A E V S Y V H V N G A K F I D
 290 300

Fig.28 Cont.

970	980	990	1000	1010	1020
1	1	1	1	1	1
CACAAATGGATTAAAGAAATCAAAACATGGCAGGGTGGTTCAGGCATGGCAAGCCATATAA					
T Q N G L R I K T W Q G G S G M A S H I					
310			320		
1030	1040	1050	1060	1070	1080
1	1	1	1	1	1
TTTATGAGAAATGTTGAAATGATAAAATTCGGAGAACCCCATATTAATAAATCAATCTACT					
I Y E N V E M I N S E N P I L I N Q F Y					
330			340		
1090	1100	1110	1120	1130	1140
1	1	1	1	1	1
GCACTTCAGCTTCTGTGCTTGCCAAACAGAGGTCTGCGGTTCAAATCCAAGATGTGACAT					
C T S A S A C Q N Q R S A V Q I Q D V T					
350			360		
1150	1160	1170	1180	1190	1200
1	1	1	1	1	1
ACAAGAACAATACGTGGGACATCAGCAACAGCAGCAGCAATTCAACTTAAGTGCAGTGACA					
Y K N I R G T S A T A A A I Q L K C S D					
370			380		

Fig. 28 Cont.

```

1210      |      1220      1230      1240      1250      1260
      |      |      |      |      |      |
GTATGCCCTGCAAAGATATAAAGCTAAGTGATATATCTTTGAAGCTTACCTCAGGAAAA
S M P C K D I K L S D I S L K L T S G K
390
1270      |      1280      1290      1300      1310      1320
      |      |      |      |      |      |
TTGCTTCCTGCCTTAATGATAAATGCAAATGGATATTTTCAGTGGACACGTCATCCCTGCAT
I A S C L N D N A N G Y F S G H V I P A
410
1330      |      1340      1350      1360      1370      1380
      |      |      |      |      |      |
GCAAGAAATTTAAGTCCAAGTGCTAAGCGAAAAGAATCTAAATCCCATAAACACCCAAAAA
C K N L S P S A K R K E S K S H K H P K
430
1390      |      1400      1410      1420      1430      1440
      |      |      |      |      |      |
CTGTAATGGTTGAAAAATATGCGAGCATATGACAAGGGTAACAGAAACACGCATATGTGTGG
T V M V E N M R A Y D K G N R T R I L L
450

```

Fig.28 Cont.

1450	1460	1470	1480	1490	1500
GGTCGAGGCCCTCCGAAATTGTACAAACAATGTCAATGGTTGCAGTCCCATGTAAGGCCAAGT					
G S R P P N C T N K C H G C S P C K A K					
470			480		
1510	1520	1530	1540	1550	1560
TAGTTATTGTTTCATCGTATTATGCCGCAGGAGTATTATCCTCAGAGGTGGATATGCAGCT					
L V I V H R I M P Q E Y Y P Q R W I C S					
490			500		
1570	1580	1590	1600	1610	1620
GTCAATGGCAAAATCTACCATCCATAATGAGATACATTGAAACTGTATGTGCTAGTGAATA					
C H G K I Y H P -					
510	514				
1630	1640	1650	1660	1670	1680
TTCTTGTGGTACAATATTAGAACTGATATTGAAAAATAAATCATCAATGTTTCTAAGGCAT					
1690	1700	1710	1720		
TTATAATAGATTATATTAATGGTTCAGCCTGGTGCAAAAAA					

Fig.28 Cont.

10	20	30	40	50
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEH				
60	70	80	90	100
SRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKK				
110	120	130	140	150
FVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTL				
160	170	180	190	200
MGKGVIDGQGKQWWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLK				
210	220	230	240	250
LMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFASKNFHLQKNT				
260	270	280	290	300
IGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVSYVHVN				
310	320	330	340	350
GAKFIDTQNGRLRIKTWQGGSGMASHIIYENVEMINSENPIILINQFYCTSA				
360	370	380	390	400
SACQNQRSQVQIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISL				
410	420	430	440	450
KLTSGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKTMV				
460	470	480	490	500
ENMRAYDKGNRTRILLGSRPPNCTNKCHGCSPCKAKLVIVHRIMPQEYYP				
510	514			
QRWICSCHGKIYHP				

Fig. 29

	50	60	
Cry j II	R K V E H S R H D A I N I F N V E K Y G A		
LONG	R K V E H S R H D A I N I F N V E K Y G A		
SHORT	S R H D A I N I F N V E K Y G A		
SAKAGUCHI	A I N I F N V E K Y		
	70	80	90
Cry j II	V G D G K H D C T E A F S T A W Q A A C K N P S		
LONG	V G D G K H D C T E A F S T A W (Q)		K N P ()
SHORT	V G D G K H D C T E A F S T A W (Q)		K N P ()

Fig 30

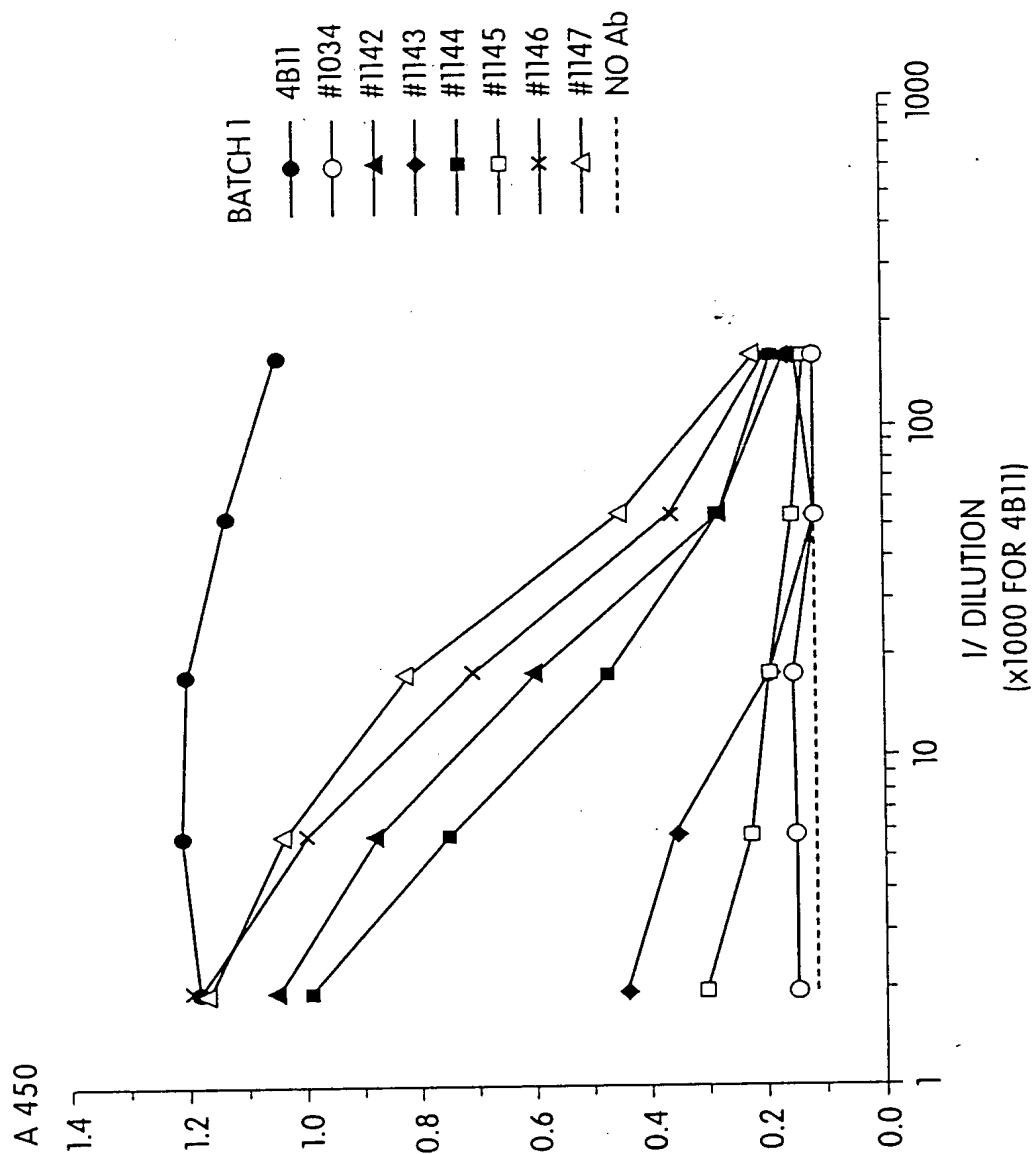


Fig. 31

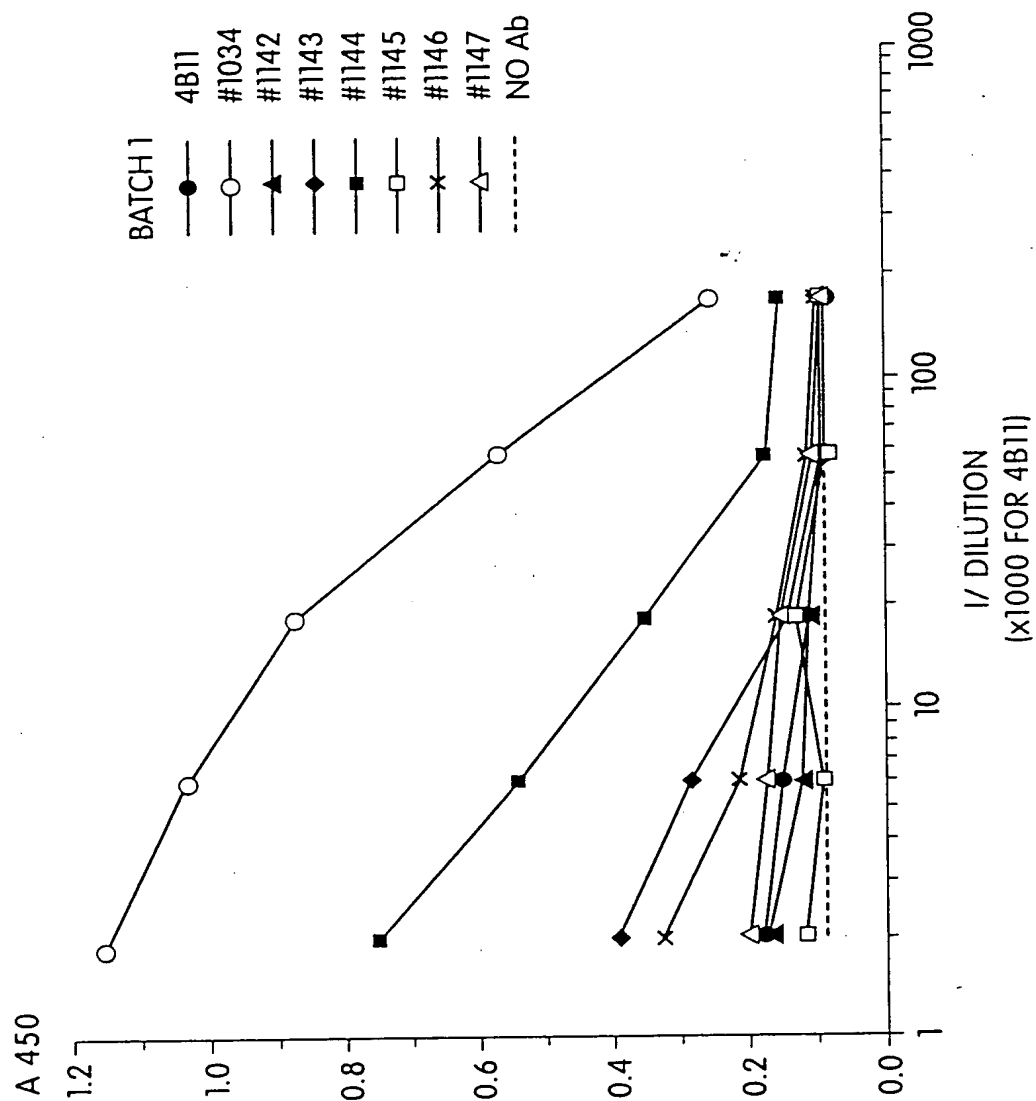


Fig. 32

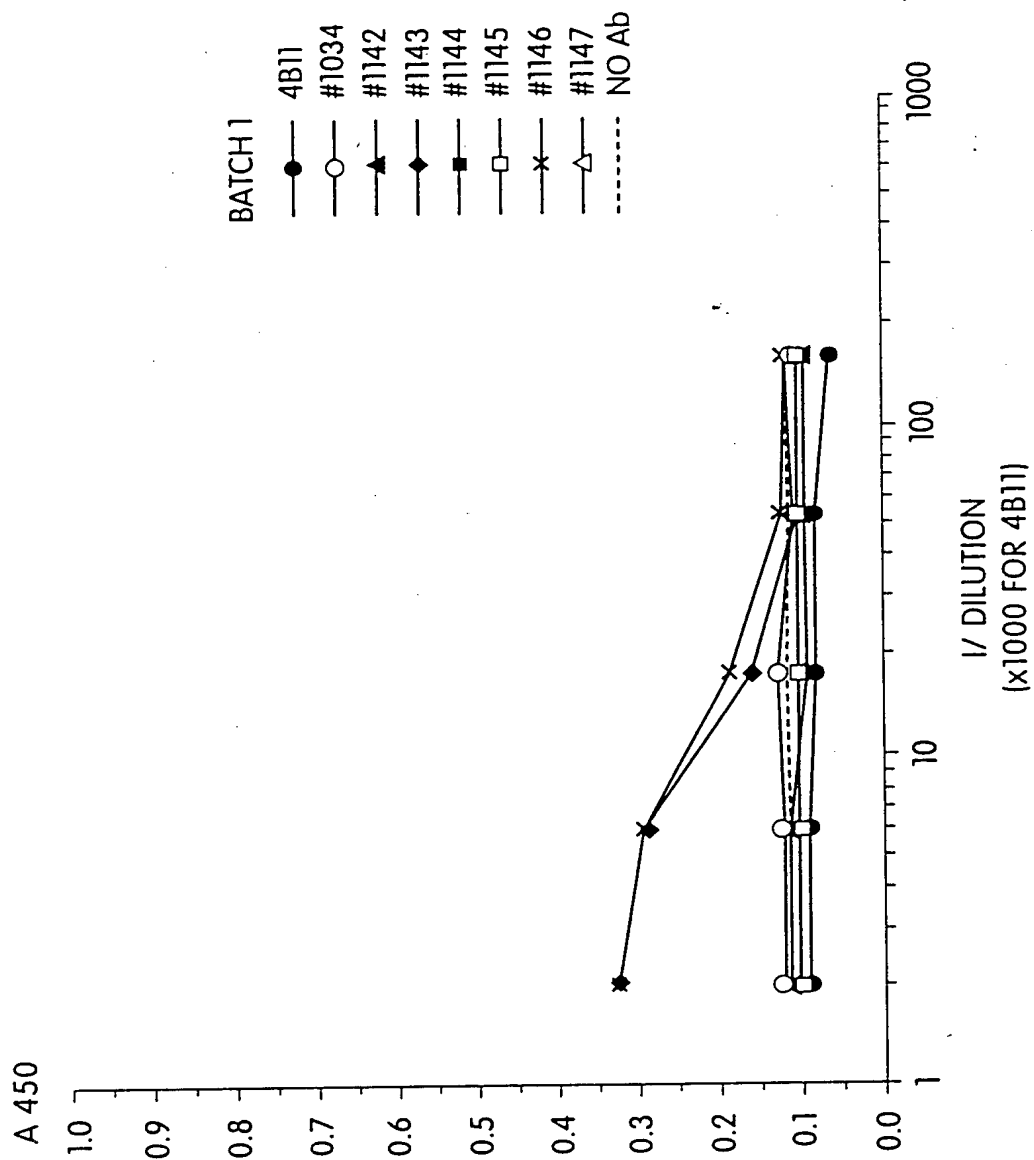


Fig. 33

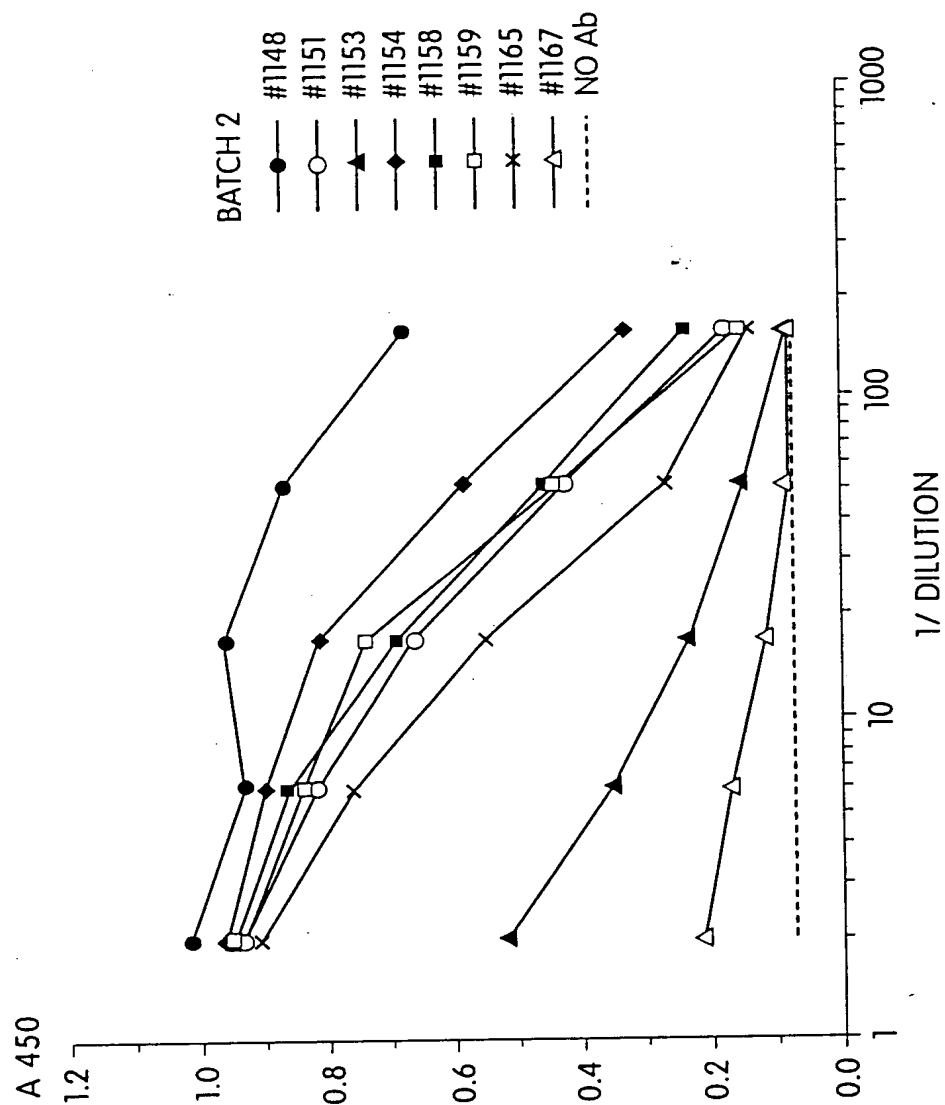


Fig. 3H

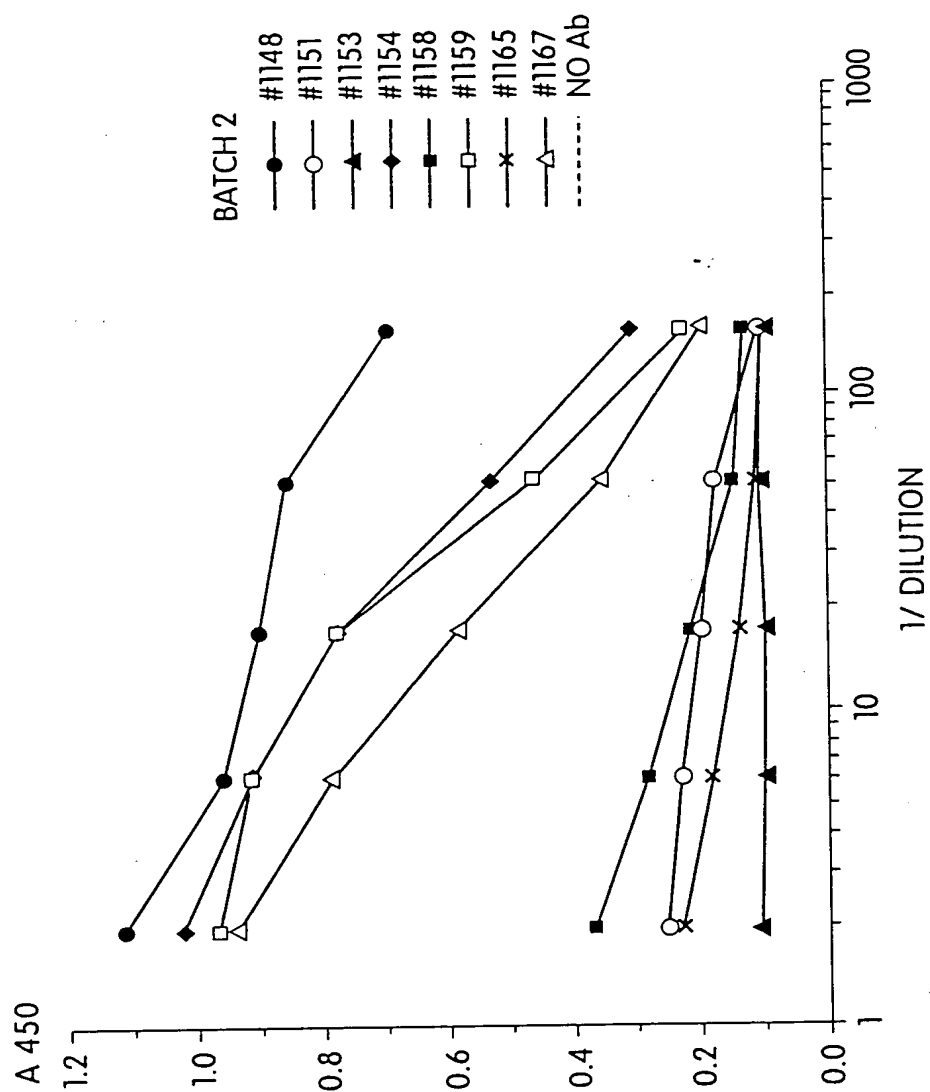


Fig. 35

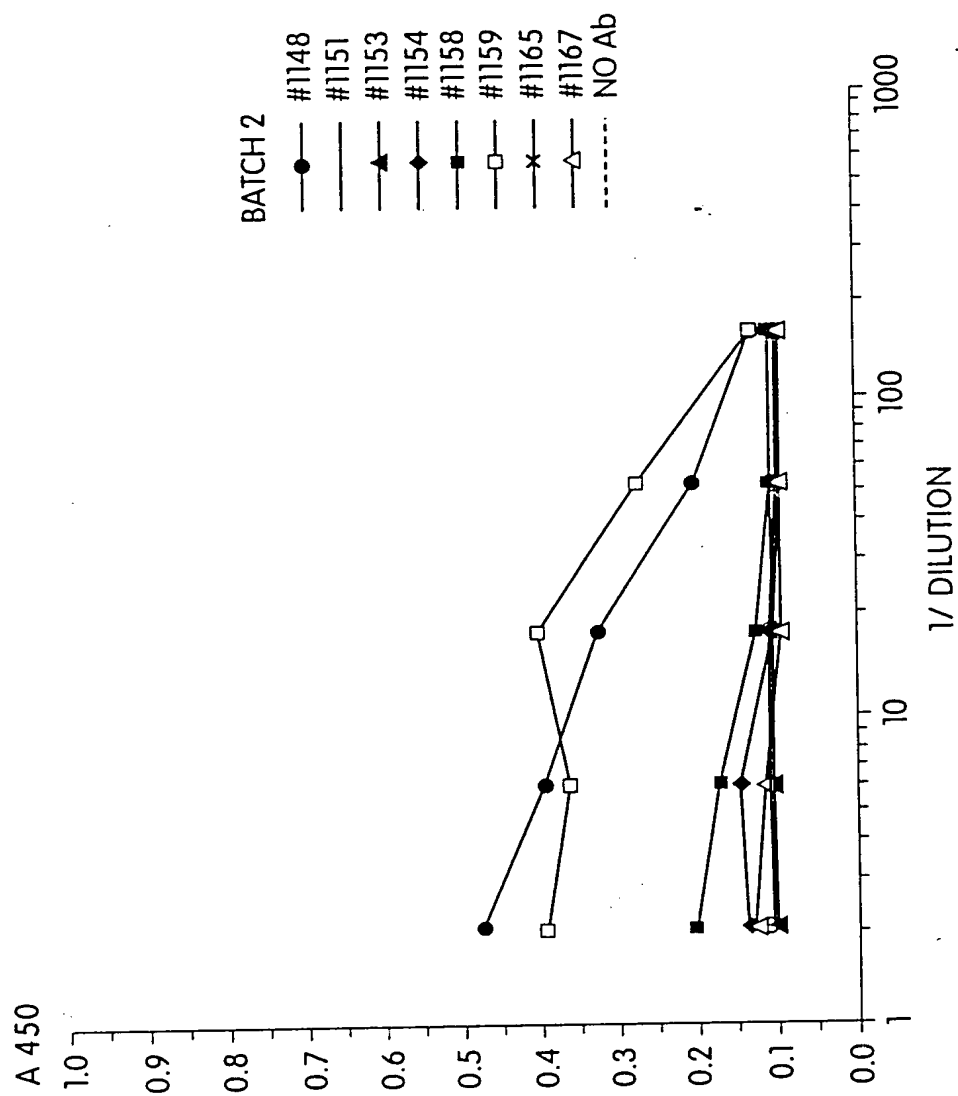


Fig. 36

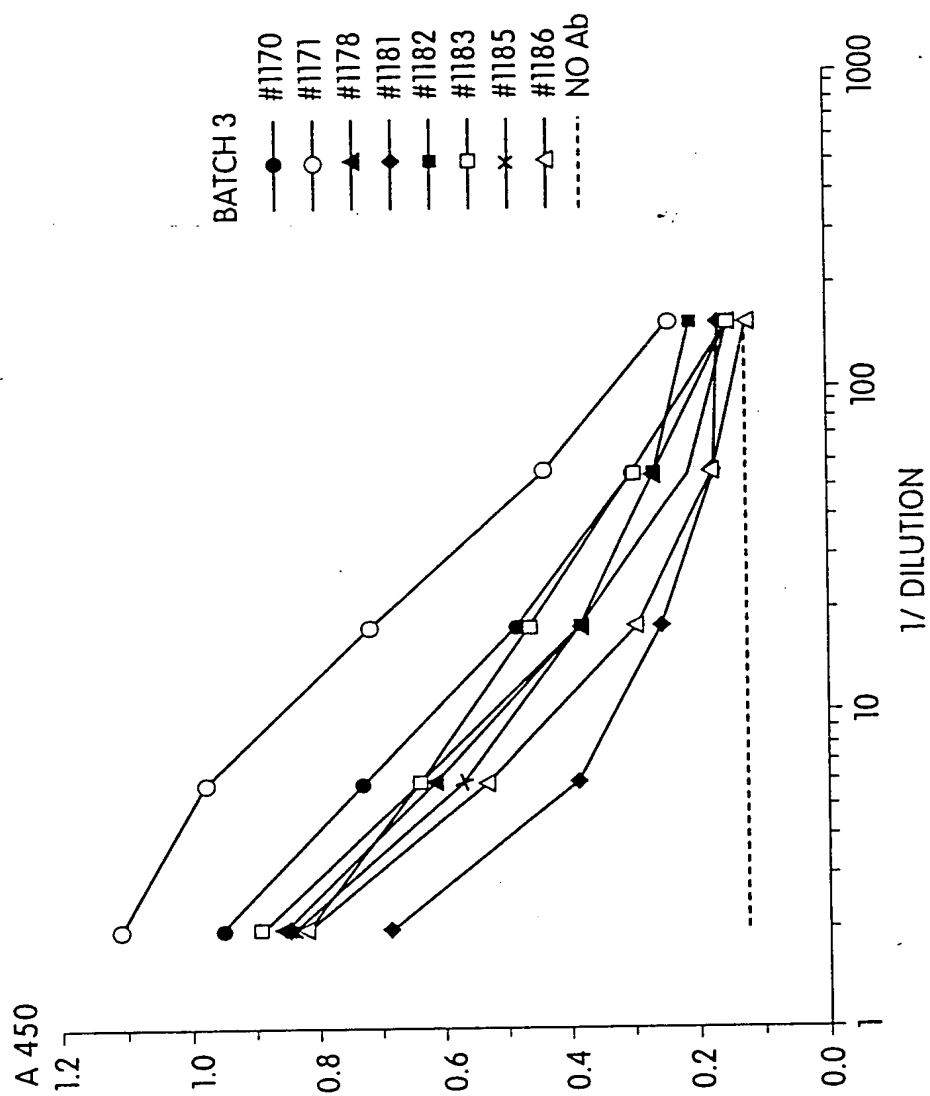


Fig. 37

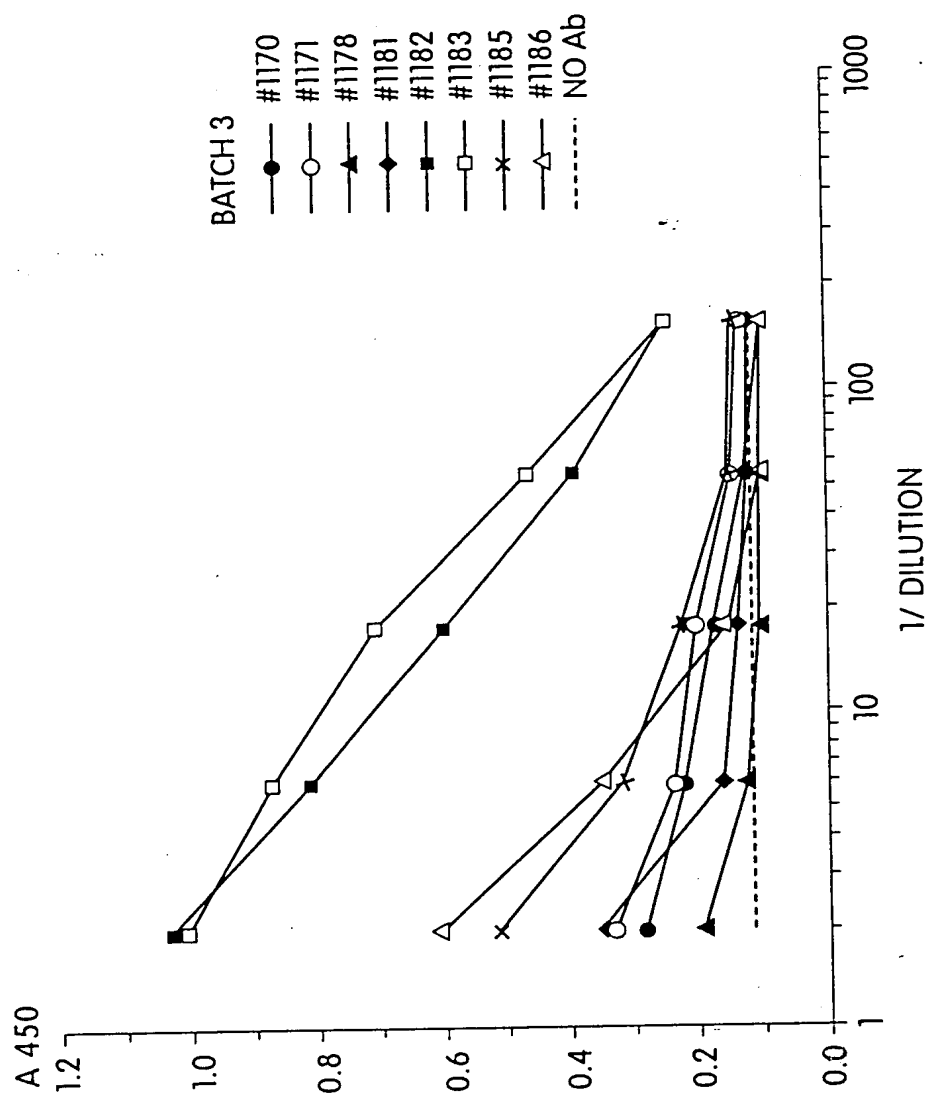


Fig. 38

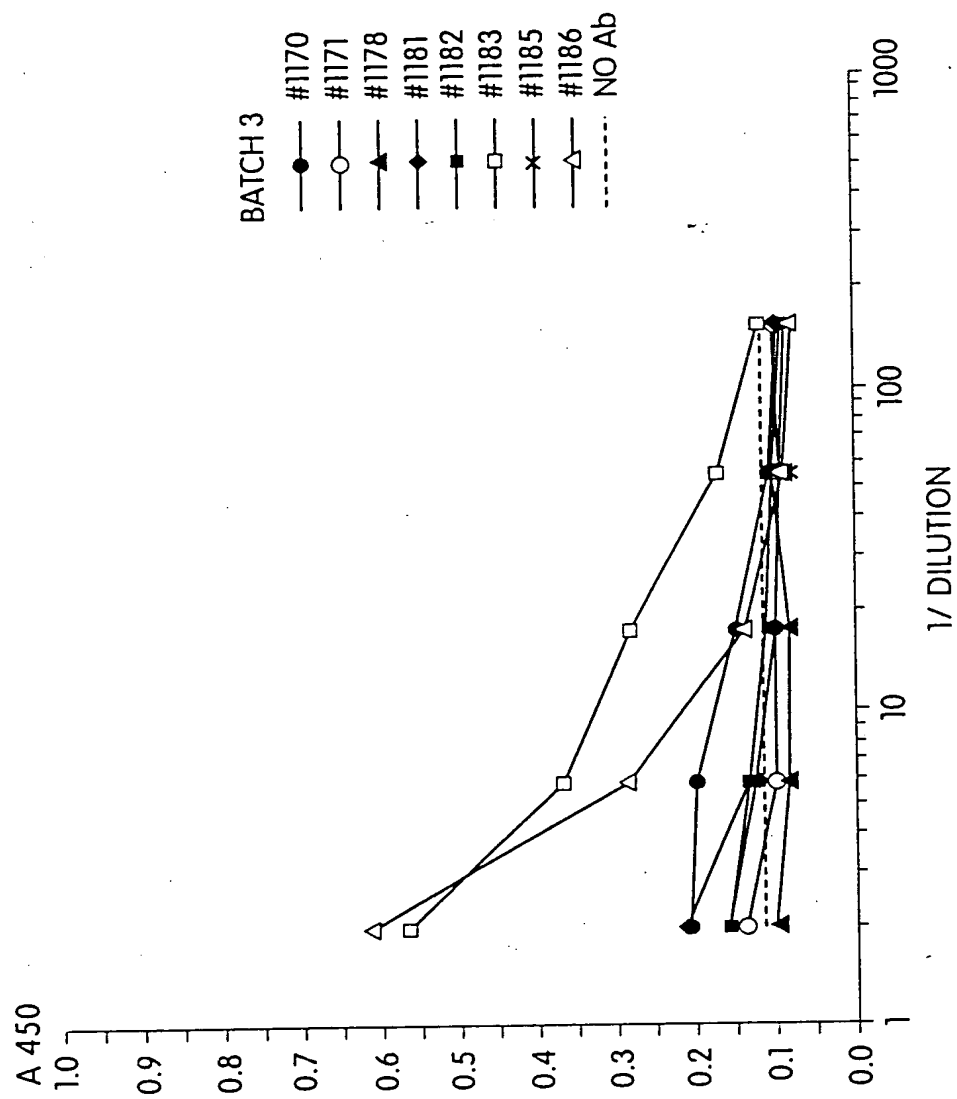


Fig. 39

PATIENT #	MAST	PURIFIED NATIVE Cry j I	PURIFIED NATIVE Cry j II	RECOMBINANT Cry j II (rCry j II)
1034	2	-	+	-
1142	2	+	-	-
1143	0	+	+	+
1144	1	+	+	-
1145	0	-	-	+
1146	3	+	-	-
1147	3	+	-	-
1148	3	+	+	+
1151	3	+	+	-
1153	1	+	-	-
1154	3	+	+	-
1158	2	+	+	-
1159	2	+	+	+
1165	1	+	-	+
1167	1/0	-	+	-
1170	1/0	+	-	-
1171	2	+	-	-
1178	1	+	-	-
1181	1/0	+	-	-
1182	1	+	+	-
1183	1	+	+	+
1185	1/0	+	+	-
1186	1/0	+	+	+
POSITIVE	21	20	13	5

Fig. 40

FIG. 41

Cry j IIA FTFKVDGIIAAYQ

Cry j IIB NGYFSGHVIPACKN

Cry j IIC:

1 10 20 30 40 50 60
| | | | | |
MGHHHHHHEFRKVEHSRHDAINIFNVEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLV
70 80 90 100 110 120
| | | | |
PGSKKFVVNNLFFNGPCQPHFTFKVDGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKGV
128
|
IDGQGKQW

Cry j IID:

1 10 20 30 40 50 60
| | | | | |
MGHHHHHHEFWAGQCKWVNGREICNDRDRPTAIKFDFSTGLIIQGLKLMNSPEFHLVFGN
70 80 90 100 110 120
| | | | |
CEGVKIIGISITAPRDSPTDGDIDIFASKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLI
127
|
CGPGHGI

Fig. 41 Cont.

Cry j IIE:

```

      1      10      20      30      40      50      60
      |      |      |      |      |      |      |
MGHHHHHHEFSIGSLGRENSRAEVSYVHVNGAKFIDTQNGRLRIKTWQGGSGMASHIIYEN
      70      80      90      100      110      120
      |      |      |      |      |      |
VEMINSENPIILINQFYCTASACQNQRSASVQIQDVTYKNIRGTSATAAAIQLKCSDSMPC
      127
      |
KDIKLS

```

Cry j IIF:

```

      1      10      20      30      40      50      60
      |      |      |      |      |      |      |
MGHHHHHHEFISLKLTSKGKIASCLNDNANGYFSGHVIPACKNLSPSAKRKESKSHKHPKT
      70      80      90      100      110      120
      |      |      |      |      |      |
VMVENMRAYDKGNRTRILLGSRPPNCTNKCHGCSPCKAKLVIVHRIMPQEYYPQRWICSC
      127
      |
HGKIYHP

```

Cry j IIG (J1) GKGVIDGQGKQWWAGQCKWVNGRE

Cry j-IIH (J3) DSMPCDKIKLSDISLKLTSKGKIAS

Cry j-IIQ (J2) IEDLICGPGHGISIGSLGRENSRA

Mean Stimulation Index

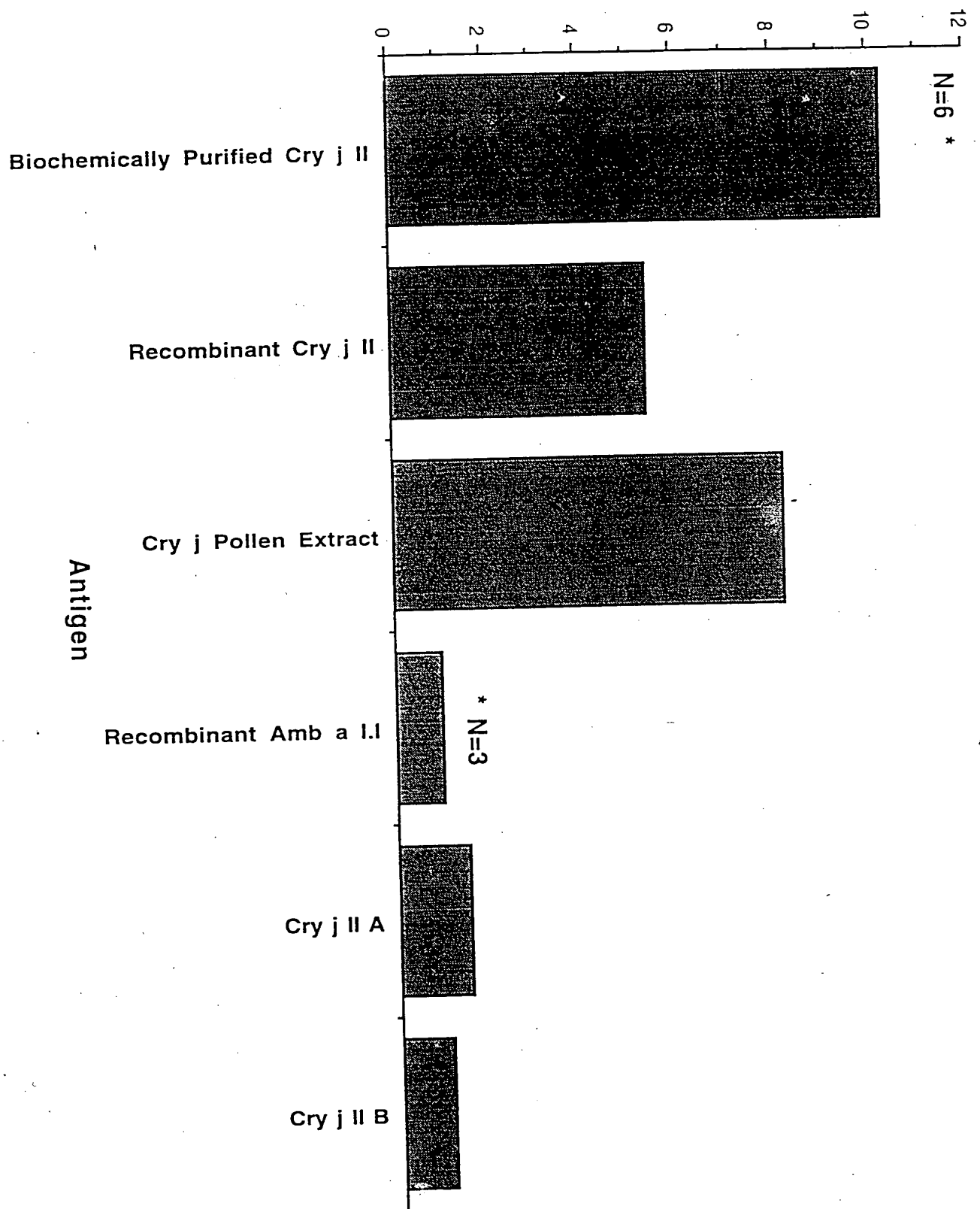


Fig 42

Fig. 43

